



#4

SEQUENCE LISTING

<110> Vernet, Corine A. M.
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Rastelli, Luca
Herrman, John L

<120> Novel Proteins and Nucleic Acids Encoding Same

<130> 15966-750

<140> 09/825,751

<141> 2001-04-03

<150> 60/194,314

<151> 2000-04-03

<150> 60/225,693

<151> 2000-08-16

<160> 85

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<222> (208)..(1698)

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tggccctgga ccctgccagc ctggggcttg ggctttgtc cccttggggc cttgagtgtg 180

gccaggcgtc tggcgattgt gtggta cag aag cca tgt ctg caa cgc ctg cca 234

Gln Lys Pro Cys Leu Gln Arg Leu Pro

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Ser Ala Asp Val Asn Glu Cys Ala Glu Asn Pro Gly Val Cys Thr Asn			
10	15	20	25
ggc gtc tgt gtc aac acc gat gga tcc ttc cgc tgt gag tgt ccc ttt			330
Gly Val Cys Val Asn Thr Asp Gly Ser Phe Arg Cys Glu Cys Pro Phe			
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ggc tac agc ctg gac ttc act ggc atc aac tgt gtg gac aca gac gag			378
Gly Tyr Ser Leu Asp Phe Thr Gly Ile Asn Cys Val Asp Thr Asp Glu			
45	50	55	
tgc tct gtc ggc cac ccc tgt ggg caa ggg aca tgc acc aat gtc atc			426
Cys Ser Val Gly His Pro Cys Gly Gln Gly Thr Cys Thr Asn Val Ile			
60	65	70	
gga ggc ttc gaa tgt gcc tgt gct gac ggc ttt gag cct ggc ctc atg			474
Gly Gly Phe Glu Cys Ala Cys Ala Asp Gly Phe Glu Pro Gly Leu Met			
75	80	85	
atg acc tgc gag gac atc gac gaa tgc tcc ctg aac ccg ctg ctc tgt			522
Met Thr Cys Glu Asp Ile Asp Glu Cys Ser Leu Asn Pro Leu Leu Cys			
90	95	100	105
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Ala Phe Arg Cys His Asn Thr Glu Gly Ser Tyr Leu Cys Thr Cys Pro			
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gcc ggc tac acc ctg cgg gag gac ggg gcc atg tgt cga gat gtg gac			618
Ala Gly Tyr Thr Leu Arg Glu Asp Gly Ala Met Cys Arg Asp Val Asp			
125	130	135	
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Glu Cys Ala Asp Gly Gln Gln Asp Cys His Ala Arg Gly Met Glu Cys			
140	145	150	
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Lys Asn Leu Ile Gly Thr Phe Ala Cys Val Cys Pro Pro Gly Met Arg			
155	160	165	
ccc ctg cct ggc tct ggg gag ggc tgc aca gat gac aat gaa tgc cac			762
Pro Leu Pro Gly Ser Gly Glu Gly Cys Thr Asp Asp Asn Glu Cys His			
170	175	180	185
gct cag cct gac ctc tgt gtc aac ggc cgc tgt gtc aac acc gcg ggc			810
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Ser Phe Arg Cys Asp Cys Asp Glu Gly Phe Gln Pro Ser Pro Thr Leu			
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acc gag tgc cac gac atc cgg cag ggg ccc tgc ttt gcc gag gtg ctg		906	
Thr Glu Cys His Asp Ile Arg Gln Gly Pro Cys Phe Ala Glu Val Leu			
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Gln Thr Met Cys Arg Ser Leu Ser Ser Ser Glu Ala Val Thr Arg			
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gcc gag tgc tgc tgt ggg ggt ggc cgg ggc tgg ggg ccc cgc tgc gag		1002	
Ala Glu Cys Cys Gly Gly Arg Gly Trp Gly Pro Arg Cys Glu			
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ctc tgt ccc ctg ccc ggc acc tct gcc tac agg aag ctg tgc ccc cat		1050	
Leu Cys Pro Leu Pro Gly Thr Ser Ala Tyr Arg Lys Leu Cys Pro His			
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Gly Ser Gly Tyr Thr Ala Glu Gly Arg Asp Val Asp Glu Cys Arg Met			
285	290	295	
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Leu Ala His Leu Cys Ala His Gly Glu Cys Ile Asn Ser Leu Gly Ser			
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Thr Cys Leu Asp Met Asp Glu Cys Ser Gln Val Pro Lys Pro Cys Thr			
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Gly Tyr Leu Leu Glu Glu Asp Gly Arg Thr Cys Lys Asp Leu Asp Glu			
365	370	375	
tgc acc tcc cgg cag cac aac tgt cag ttc ctc tgt gtc aac act gtg		1386	
Cys Thr Ser Arg Gln His Asn Cys Gln Phe Leu Cys Val Asn Thr Val			
380	385	390	

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Gly Ala Phe Thr Cys Arg Cys Pro Pro Gly Phe Thr Gln His His Gln			
395	400	405	
gcc tgc ttc gac aat gat gag tgc tca gcc cag cct ggc cca tgt ggt			1482
Ala Cys Phe Asp Asn Asp Glu Cys Ser Ala Gln Pro Gly Pro Cys Gly			
410	415	420	425
gcc cac ggg cac tgc cac aac acc ccg ggc agc ttc cgc tgt gaa tgc			1530
Ala His Gly His Cys His Asn Thr Pro Gly Ser Phe Arg Cys Glu Cys			
430	435	440	
cac caa ggc ttc acc ctg gtc agc tca ggc cat ggc tgt gaa gat gtg			1578
His Gln Gly Phe Thr Leu Val Ser Ser Gly His Gly Cys Glu Asp Val			
445	450	455	
aat gaa tgt gat ggg ccc cac cgc tgc cag cat ggc tgt cag aac cag			1626
Asn Glu Cys Asp Gly Pro His Arg Cys Gln His Gly Cys Gln Asn Gln			
460	465	470	
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Leu Gly Gly Tyr Arg Cys Ser Cys Pro Gln Gly Phe Thr Gln His Ser			
475	480	485	
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Gln Trp Ala Gln Cys Val Gly Glu			
490	495		
caccagaatc tgctcagagc aggccactaa cagacgccac cctgcaagat gatgtgacaa			1788
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gccc			1852

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Ala Asp Gly Phe Glu Pro Gly Leu Met Met Thr Cys Glu Asp Ile Asp		
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Glu Cys Ser Leu Asn Pro Leu Leu Cys Ala Phe Arg Cys His Asn Thr		
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Glu Gly Ser Tyr Leu Cys Thr Cys Pro Ala Gly Tyr Thr Leu Arg Glu		
115	120	125
Asp Gly Ala Met Cys Arg Asp Val Asp Glu Cys Ala Asp Gly Gln Gln		
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Asp Cys His Ala Arg Gly Met Glu Cys Lys Asn Leu Ile Gly Thr Phe		
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Ala Cys Val Cys Pro Pro Gly Met Arg Pro Leu Pro Gly Ser Gly Glu		
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Gly Cys Thr Asp Asp Asn Glu Cys His Ala Gln Pro Asp Leu Cys Val		
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195	200	205
Glu Gly Phe Gln Pro Ser Pro Thr Leu Thr Glu Cys His Asp Ile Arg		
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Gln Gly Pro Cys Phe Ala Glu Val Leu Gln Thr Met Cys Arg Ser Leu		
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245	250	255
Gly Arg Gly Trp Gly Pro Arg Cys Glu Leu Cys Pro Leu Pro Gly Thr		
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Gly Arg Asp Val Asp Glu Cys Arg Met Leu Ala His Leu Cys Ala His		

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Gly Glu Cys Ile Asn Ser Leu Gly Ser Phe Arg Cys His Cys Gln Ala		
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325	330	335
Cys Ser Gln Val Pro Lys Pro Cys Thr Phe Leu Cys Lys Asn Thr Lys		
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Gly Ser Phe Leu Cys Ser Cys Pro Arg Gly Tyr Leu Leu Glu Glu Asp		
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385	390	395
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Ser Ser Gly His Gly Cys Glu Asp Val Asn Glu Cys Asp Gly Pro His		
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Arg Cys Gln His Gly Cys Gln Asn Gln Leu Gly Gly Tyr Arg Cys Ser		
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cgg	gcc	ttc	aat	gcg	aag	cct	gct	gcc	acc	atc	atc	tgg	ttc	cgg	96	
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gac

ggg	acg	cag	cag	gag	ggc	gct	gtg	gcc	agc	acg	gaa	ttg	ctg	aag	144	
Asp	Gly	Thr	Gln	Gln	Glu	Gly	Ala	Val	Ala	Ser	Thr	Glu	Leu	Leu	Lys	
35										40					45	

gat

ggg	aag	agg	gag	acc	acc	gtg	agc	caa	ctg	ctt	att	aac	ccc	acg	192	
Asp	Gly	Lys	Arg	Glu	Thr	Thr	Val	Ser	Gln	Leu	Ile	Asn	Pro	Thr		
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gac

ctg	gac	ata	ggg	cgt	gtc	ttc	act	tgc	cga	agc	atg	aac	gaa	gcc	240	
Asp	Leu	Asp	Ile	Gly	Arg	Val	Phe	Thr	Cys	Arg	Ser	Met	Asn	Glu	Ala	
65										75					80	

atc

cct	agt	ggc	aag	gag	act	tcc	atc	gag	ctg	gat	gtg	cac	cac	cct	288	
Ile	Pro	Ser	Gly	Lys	Glu	Thr	Ser	Ile	Glu	Leu	Asp	Val	His	His	Pro	
85										90					95	

cct

aca	gtg	acc	ctg	tcc	att	gag	cca	cag	acg	ggg	cag	gag	ggt	gag	336	
Pro	Thr	Val	Thr	Leu	Ser	Ile	Glu	Pro	Gln	Thr	Gly	Gln	Glu	Gly	Glu	
100										105					110	

cgt

gtt	gtc	ttt	acc	tgc	cag	gcc	aca	gcc	aac	ccc	gag	atc	t		379	
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Cys

Arg	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Ala	Thr	Ile	Ile	Trp	Phe	Arg	
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20 25 30

Asp Gly Thr Gln Gln Glu Gly Ala Val Ala Ser Thr Glu Leu Leu Lys
35 40 45

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50 55 60

Asp Leu Asp Ile Gly Arg Val Phe Thr Cys Arg Ser Met Asn Glu Ala
65 70 75 80

Ile Pro Ser Gly Lys Glu Thr Ser Ile Glu Leu Asp Val His His Pro
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Cys Pro Val Gly His Arg Leu Ser Asp Ser Ser Ala Ala Cys Glu Asp
20 25 30

tac cgg gcc ggc gcc tgc ttc tca gtg ctt ttc ggg ggc cgc tgt gct 143
Tyr Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala
35 40 45

gga gac ctc gcc ggc cac tac act cgc agg cag tgc tgc tgt gac agg 191
Gly Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg
50 55 60

ggc agg tgc tgg gca gct ggc ccg gtc cct gag ctg tgt cct cct cgg			239
Gly Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg			
65	70	75	
ggc tcc aat gaa ttc cag caa ctg tgc gcc cag cgg ctg cct cta			287
Gly Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu			
80	85	90	95
ccc ggc cac cct ggc ctc ttc cct ggc ctc ctg ggc ttc gga tcc aat			335
Pro Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn			
100	105	110	
ggc atg ggt ccc cct ctt ggg cca gcg cga ctc aac ccc cat ggc tct			383
Gly Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser			
115	120	125	
gat gcg cgt ggg atc ccc agc ctg ggc cct ggc aac tct aat att ggc			431
Asp Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly			
130	135	140	
act gct acc ctg aac cag acc att gac atc tgc cga cac ttc acc aac			479
Thr Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn			
145	150	155	
ctg tgt ctg aat ggc cgc tgc ctg ccc acg cct tcc agc tac cgc tgc			527
Leu Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys			
160	165	170	175
gag tgt aac gtg ggc tac acc cag gac gtg cgc ggc gag tgc att gat			575
Glu Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp			
180	185	190	
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Val Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn			
195	200	205	
atc ccc ggc acc tac cac tgc cgg tgc tac ccg ggc ttc cag gcc acg			671
Ile Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr			
210	215	220	
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Pro Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly			
225	230	235	
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Gly Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln			
240	245	250	255

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Cys Val Cys Asn Ala Gly Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys			
260	265	270	
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Val Asp His Asn Glu Cys Ala Thr Ser Thr Met Cys Val Asn Gly Val			
275	280	285	
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Cys Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe			
290	295	300	
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Leu Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln			
305	310	315	
acg ccc ggc atc tgc gtg aac ggc cac tgt acc aac acc gag ggc tcc			1007
Thr Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser			
320	325	330	335
ttc cgc tgc cag tgc ctg ggg ggg ctg gcg gta ggc acg gat ggc cgc			1055
Phe Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg			
340	345	350	
gtg tgc gtg gac acc cac gtg cgc agc acc tgc tat ggg gcc atc gag			1103
Val Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu			
355	360	365	
aag ggc tcc tgt gcc cgc ccc ttc cct ggc act gtc acc aag tcg gag			1151
Lys Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu			
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Cys Cys Cys Ala Asn Pro Asp His Gly Phe Gly Glu Pro Cys Gln Leu			
385	390	395	
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Cys Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly			
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Leu Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp			
420	425	430	
cct gag gtt tgt gcc aat ggc gtg tgc gag aac ctt cgg ggc agc tac			1343
Pro Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr			
435	440	445	

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Cys Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn			
465	470	475	
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Gly Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro			
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Gly Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu			
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Cys Leu Ser Ser Pro Cys Val Ser Gly Val Cys Arg Asn Leu Ala Gly			
515	520	525	
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Ser Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly			
530	535	540	
acc ttc tgt cta gac agc acc aag ggc acc tgc tgg ctg aag atc cag			1679
Thr Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln			
545	550	555	
gag agc cgc tgt gag gtg aac ctt cag gga gcc agc ctg cgg tct gag			1727
Glu Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu			
560	565	570	575
tgc tgt gcc acc ctc ggg gca gcc tgg ggg agc ccc tgc gaa cgc tgc			1775
Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys			
580	585	590	
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Glu Ile Asp Pro Ala Cys Ala Arg Gly Phe Ala Arg Met Thr Gly Val			
595	600	605	
acc tgc gat gat gtg aac gag tgt gag tcc ttc ccg gga gtc tgt ccc			1871
Thr Cys Asp Asp Val Asn Glu Cys Glu Ser Phe Pro Gly Val Cys Pro			
610	615	620	
aac ggg cgt tgc gtc aac act gct ggg tct ttc cgc tgt gag tgt cca			1919
Asn Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Glu Cys Pro			
625	630	635	

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Glu Gly Leu Met Leu Asp Ala Ser Gly Arg Leu Cys Val Asp Val Arg			
640	645	650	655
ttg gaa cca tgt ttc ctg cga tgg gat gag gat gag tgt ggg gtc acc			2015
Leu Glu Pro Cys Phe Leu Arg Trp Asp Glu Asp Glu Cys Gly Val Thr			
660	665	670	
ctg cct ggc aag tac cgg atg gac gtc tgc tgc tcc atc ggg gcc			2063
Leu Pro Gly Lys Tyr Arg Met Asp Val Cys Cys Ser Ile Gly Ala			
675	680	685	
gtg tgg gga gtc gag tgc gag gcc tgc ccg gat ccc gag tct ctg gag			2111
Val Trp Gly Val Glu Cys Glu Ala Cys Pro Asp Pro Glu Ser Leu Glu			
690	695	700	
ttc gcc agc ctg tgc ccg cgg ggg ctg ggc ttc gcc agc ccg gac ttc			2159
Phe Ala Ser Leu Cys Pro Arg Gly Leu Gly Phe Ala Ser Arg Asp Phe			
705	710	715	
ctg tct ggc cga cca ttc tat aaa gat gtg aat gaa tgc aag gtg ttc			2207
Leu Ser Gly Arg Pro Phe Tyr Lys Asp Val Asn Glu Cys Lys Val Phe			
720	725	730	735
cct ggc ctc tgc acg cac ggt acc tgc aga aac acg gtg ggc agc ttc			2255
Pro Gly Leu Cys Thr His Gly Thr Cys Arg Asn Thr Val Gly Ser Phe			
740	745	750	
cac tgc gcc tgt gcg ggg ggc ttc gcc ctg gat gcc cag gaa cgg aac			2303
His Cys Ala Cys Ala Gly Gly Phe Ala Leu Asp Ala Gln Glu Arg Asn			
755	760	765	
tgc aca gat atc gac gag tgt cgc atc tct cct gac ctc tgc ggc cag			2351
Cys Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Gln			
770	775	780	
ggc acc tgt gtc aac acg ccg ggc agc ttt gag tgc gag tgt ttt ccc			2399
Gly Thr Cys Val Asn Thr Pro Gly Ser Phe Glu Cys Glu Cys Phe Pro			
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gag tgt gca agg gac ccg ctg ctc tgc cgg gga ggc act tgc acc aac			2495
Glu Cys Ala Arg Asp Pro Leu Leu Cys Arg Gly Gly Thr Cys Thr Asn			
820	825	830	

acg gat ggg agc tac aag tgc cag tgt ccc cct ggg cat gag ctg acg			2543
Thr Asp Gly Ser Tyr Lys Cys Gln Cys Pro Pro Gly His Glu Leu Thr			
835	840	845	
gcc aag ggc act gcc tgt gag gac atc gag tgc tcc ctg agt gat			2591
Ala Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp			
850	855	860	
ggc ctg tgt ccc cat ggc cag tgt gtc aat gtc atc ggt gcc ttc cag			2639
Gly Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln			
865	870	875	
tgc tcc tgc cat gcc ggc ttc cag agc aca cct gac cgc cag ggc tgc			2687
Cys Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys			
880	885	890	895
gtg gac atc aac gaa tgc cgg gtc cag aat ggt ggg tgt gac gtg cac			2735
Val Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His			
900	905	910	
cgt att aac act gag ggc agc tac cgg tgc agc tgt ggg cag ggc tac			2783
Arg Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr			
915	920	925	
tcg ctg atg ccc gac gga agg gca tgt gca gac gtg gac gag tgt gaa			2831
Ser Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu			
930	935	940	
gag aac ccc cgc gtt tgt gac caa ggc cac tgc acc aac atg cca ggg			2879
Glu Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly			
945	950	955	
tgt cac cgc tgc ctg tgc tat gat ggc ttc atg gcc acg cca gac atg			2927
Gly His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met			
960	965	970	975
agg aca tgt gtt gat gtg gat gag tgt gac ctg aac cct cac atc tgc			2975
Arg Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys			
980	985	990	
ctc cat ggg gac tgc gag aac acg aag ggt tcc ttt gtc tgc cac tgt			3023
Leu His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys			
995	1000	1005	
cag ctg ggc tac atg gtc agg aag ggg gcc aca ggc tgc tct gat gtg			3071
Gln Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val			
1010	1015	1020	

gat gaa tgc gag gtt gga gga cac aac tgt gac agt cac gcc tcc tgt			3119
Asp Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys			
1025	1030	1035	
ctc aac atc ccg ggg agt ttc agc tgt agg tgc ctg cca ggc tgg gtg			3167
Leu Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val			
1040	1045	1050	1055
ggg gat ggc ttc gaa tgt cac gac ctg gat gaa tgc gtc tcc cag gag			3215
Gly Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu			
1060	1065	1070	
cac cg ^g tgc agc cca aga ggt gac tgt ctc aat gtc cct ggc tcc tac			3263
His Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr			
1075	1080	1085	
cgc tgc acc tgc cgc cag ggc ttt gcc ggg gat ggc ttc ttc tgc gaa			3311
Arg Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu			
1090	1095	1100	
gac agg gat gaa tgt gcc gag aac gtg gac ctc tgt gac aac ggg			3356
Asp Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly			
1105	1110	1115	
tagtgccctca atgcgcc			3374

<210> 6
<211> 1118
<212> PRT
<213> Homo sapiens

<400> 6			
Gln Gly Gly Ser Cys Val Asn Met Val Gly Ser Phe His Cys Arg Cys			
1	5	10	15
Pro Val Gly His Arg Leu Ser Asp Ser Ser Ala Ala Cys Glu Asp Tyr			
20	25	30	
Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala Gly			
35	40	45	
Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg Gly			
50	55	60	
Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg Gly			
65	70	75	80

Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro
85 90 95

Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly
100 105 110

Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp
115 120 125

Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr
130 135 140

Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu
145 150 155 160

Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu
165 170 175

Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val
180 185 190

Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn Ile
195 200 205

Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro
210 215 220

Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly
225 230 235 240

Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys
245 250 255

Val Cys Asn Ala Gly Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val
260 265 270

Asp His Asn Glu Cys Ala Thr Ser Thr Met Cys Val Asn Gly Val Cys
275 280 285

Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe Leu
290 295 300

Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln Thr
305 310 315 320

Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser Phe
325 330 335

Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg Val
340 345 350

Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu Lys
355 360 365

Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu Cys
370 375 380

Cys Cys Ala Asn Pro Asp His Gly Phe Gly Glu Pro Cys Gln Leu Cys
385 390 395 400

Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly Leu
405 410 415

Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp Pro
420 425 430

Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr Arg
435 440 445

Cys Val Cys Asn Leu Gly Tyr Glu Ala Gly Ala Ser Gly Lys Asp Cys
450 455 460

Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn Gly
465 470 475 480

Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro Gly
485 490 495

Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu Cys
500 505 510

Leu Ser Ser Pro Cys Val Ser Gly Val Cys Arg Asn Leu Ala Gly Ser
515 520 525

Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr
530 535 540

Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln Glu
545 550 555 560

Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu Cys
565 570 575

Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys Glu
580 585 590

Ile Asp Pro Ala Cys Ala Arg Gly Phe Ala Arg Met Thr Gly Val Thr
595 600 605

Cys Asp Asp Val Asn Glu Cys Glu Ser Phe Pro Gly Val Cys Pro Asn
610 615 620

Gly Arg Cys Val Asn Thr Ala Gly Ser Phe Arg Cys Glu Cys Pro Glu
625 630 635 640

Gly Leu Met Leu Asp Ala Ser Gly Arg Leu Cys Val Asp Val Arg Leu
645 650 655

Glu Pro Cys Phe Leu Arg Trp Asp Glu Asp Glu Cys Gly Val Thr Leu
660 665 670

Pro Gly Lys Tyr Arg Met Asp Val Cys Cys Cys Ser Ile Gly Ala Val
675 680 685

Trp Gly Val Glu Cys Glu Ala Cys Pro Asp Pro Glu Ser Leu Glu Phe
690 695 700

Ala Ser Leu Cys Pro Arg Gly Leu Gly Phe Ala Ser Arg Asp Phe Leu
705 710 715 720

Ser Gly Arg Pro Phe Tyr Lys Asp Val Asn Glu Cys Lys Val Phe Pro
725 730 735

Gly Leu Cys Thr His Gly Thr Cys Arg Asn Thr Val Gly Ser Phe His
740 745 750

Cys Ala Cys Ala Gly Gly Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys
755 760 765

Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly
770 775 780

Thr Cys Val Asn Thr Pro Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly
785 790 795 800

Tyr Glu Ser Gly Phe Met Leu Met Lys Asn Cys Met Asp Val Asp Glu
805 810 815

Cys Ala Arg Asp Pro Leu Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr
820 825 830

Asp Gly Ser Tyr Lys Cys Gln Cys Pro Pro Gly His Glu Leu Thr Ala
835 840 845

Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly
850 855 860

Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln Cys
865 870 875 880

Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys Val
885 890 895

Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His Arg
900 905 910

Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser
915 920 925

Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu Glu
930 935 940

Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly Gly
945 950 955 960

His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met Arg
965 970 975

Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys Leu
980 985 990

His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys Gln
995 1000 1005

Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val Asp
1010 1015 1020

Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys Leu
1025 1030 1035 1040

Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val Gly
1045 1050 1055

Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu His
1060 1065 1070

Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr Arg
1075 1080 1085

Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu Asp
1090 1095 1100

Arg Asp Glu Cys Ala Glu Asn Val Asp Leu Cys Asp Asn Gly
1105 1110 1115

<210> 7
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(292)

<400> 7
t cac ggg aat aag cct ggg ccc gtc cct ttg att tcc aac aag atc tgc 49
His Gly Asn Lys Pro Gly Pro Val Pro Leu Ile Ser Asn Lys Ile Cys
1 5 10 15

aac cac agg gac gtg tac ggt ggc atc atc tcc ccc tcc atg ctc tgc 97
Asn His Arg Asp Val Tyr Gly Ile Ile Ser Pro Ser Met Leu Cys
20 25 30

gcg ggc tac ctg acg ggt ggc gtg gac agc tgc cag ggg gac agc ggg 145
Ala Gly Tyr Leu Thr Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
35 40 45

ggg ccc ctg gtg tgt caa gag agg ctg tgg aag tta gtg gga gcg 193
Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala
50 55 60

acc agc ttt ggc atc ggc tgc gca gag gtg aac aag cct ggg gtg tac 241
Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr
65 70 75 80

acc gtg tca cct cct tcc tgg act gga tcc acg agc aga tgg aga gag 289
Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu
85 90 95

acc taaaaacctg aagaggaagg ggataagtag ccacctgagt tcctgaggtg 342
Thr

atgaagacag cccgatcctc ccctggactc ccgtgttagga acctgcacac gagcagacac 402

cottggagct ctgagttccg gcaccagtag caggccc 439

<210> 8

<211> 97
<212> PRT
<213> Homo sapiens

<400> 8

His Gly Asn Lys Pro Gly Pro Val Pro Leu Ile Ser Asn Lys Ile Cys

1 5 10 15

Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu Cys
20 25 30

Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
35 40 45

Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala
50 55 60

Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr
65 70 75 80

Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu
85 90 95

Thr

<210> 9
<211> 410
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(410)

<400> 9

tg tca ttg tcc ttt tac cta tta tat ttt ttc ata ctc tgt gaa aac 47
Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
1 5 10 15

aaa tca gtt gcc gga cta acc atg acc tat gat gga aat aat cca gtg 95
Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
20 25 30

aca tct cat aga gat gtg cca ctt tct tat tgc aac tca gac tgc aat 143
Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn

35

40

45

tgt gat gaa agt cag tgg gaa cca gtc tgt ggg aac aat gga ata act 191
 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
 50 55 60

tac ctg tca cct tgt cta gca gga tgc aaa tcc tca agt ggt att aaa 239
 Tyr Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys
 65 70 75

aag cat aca gtg ttt tat aac tgt agt tgt gtg gaa gta act ggt ctc 287
 Lys His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu
 80 85 90 95

cag aac aga aat tac tca gcg cac ttg ggt gaa tgc cca aga gat aat 335
 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn
 100 105 110

act tgt aca agg aaa ttt ttc atc tat gtt gca att caa gtc ata aac 383
 Thr Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn
 115 120 125

tct ttg ttc tct gca aca gga ggt acc 410
 Ser Leu Phe Ser Ala Thr Gly Gly Thr
 130 135

<210> 10
<211> 136
<212> PRT
<213> Homo sapiens

<400> 10
Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys
 1 5 10 15

Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr
 20 25 30

Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys
 35 40 45

Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr
 50 55 60

Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys Lys
 65 70 75 80

His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu Gln
85 90 95

Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn Thr
100 105 110

Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn Ser
115 120 125

Leu Phe Ser Ala Thr Gly Gly Thr
130 135

<210> 11
<211> 322
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)...(320)

<400> 11
tg gca gcc ctg gag gag ccg atg gtg gac ctg gac ggc gag ctg cct 47
Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
1 5 10 15

ttc gtg cggttcccctgccccacattgccgtgctccaggacgatctggcc 95
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
20 25 30

caa ctc ttc cag gat gac gac gtc ggg gcc gat gag gaa gag gca gag 143
Gln Leu Phe Gln Asp Asp Val Gly Ala Asp Glu Glu Ala Glu
35 40 45

ttg cgg ggc gaa cac acg ctc aca gag aag ttt gtc tgc ctg gat gac 191
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
50 55 60

tcc ttt ggc cat gac tgc agc ttg acc tgt gat gac tgc agg aac gga 239
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65 70 75

ggg acc tgc ctc ctg ggc ctg gat ggc tgt gat tgc ccc gag ggg tgg 287
Gly Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp
80 85 90 95

act ggg gtt att tgc aat gag att tgt cct ccg ga 322
Thr Gly Val Ile Cys Asn Glu Ile Cys Pro Pro
100 105

<210> 12
<211> 106
<212> PRT
<213> Homo sapiens

<400> 12
Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro Phe
1 5 10 15

Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro Gln
20 25 30

Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Ala Glu Leu
35 40 45

Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp Ser
50 55 60

Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly Gly
65 70 75 80

Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp Thr
85 90 95

Gly Val Ile Cys Asn Glu Ile Cys Pro Pro
100 105

<210> 13
<211> 1332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)...(1306)

<400> 13
c gcc ttc atg ctg ccg gcg ggc tgc tcg cgc cgg ctg gtg gcc gag ctg 49
Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu
1 5 10 15

cag ggc gcc ctg gac gcc tgc gca cag cga caa ttg caa ttg gag cag		97	
Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln			
20	25	30	
agc ctg cgc gtt tgc cgt cg ^g ctg cat gcc tgg gaa cca act ggg		145	
Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly			
35	40	45	
acc cgg gct ttg aag cca cct cca ggg cca gaa act aat gga gag gac		193	
Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp			
50	55	60	
ccc ctt cca gca tgc aca ccc agt cca caa gac ctc aaa gag ttg gag		241	
Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu			
65	70	75	80
ttt ctg acc cag gca ctg gag aag gct gta cga gtt cga aga ggc atc		289	
Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile			
85	90	95	
act aag gcc gaa gag aga gac aag gcc ccc agc ctg aaa tct agg tcc		337	
Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser			
100	105	110	
att gtc acc tct tct ggc acg aca gcc tcc gcc cca ccg cat tcc cca		385	
Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro			
115	120	125	
ggc caa gct ggt ggc cat gct tca gac acg aga ccc acc aag ggc ctc		433	
Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu			
130	135	140	
cgc cag acc acg gtg cct gcc aag ggc cac cct gag cgc ccg ctg ctg		481	
Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu			
145	150	155	160
tca gtg ggg gat ggg acc cgt gtt ggg atg gga gcc cga acc ccc agg		529	
Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg			
165	170	175	
cct ggg gcg ggc ctc agg gac cag caa atg gcc cca tcc gct gct cct		577	
Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro			
180	185	190	
cag gcc cca gaa gcc ttc aca ctc aag gag aag ggg cac ctg ctg ccg		625	
Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg			
195	200	205	

ctg cct gca ttc agg aaa gca gct tcc cag aac tcg agc ctg tgg			673
Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp			
210	215	220	
gcc cag ctc agt tcc aca cag acc agt gat tcc acg gat gcc gcc gct			721
Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala			
225	230	235	240
gcc aaa acc cag ttc ctc cag aac atg cag aca gct tca ggc ggg ccc			769
Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro			
245	250	255	
cag ccc agg ctc agt gct gtg gag gtg gag gcg gag gcg ggg cgc ctg			817
Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu			
260	265	270	
cgg aag gcc tgc tcg ctg aga ctg cgc atg agg gag gag ctc tca			865
Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser			
275	280	285	
gca gcc ccc atg gac tgg atg cag gag tac cgc tgc ctg ctc acg ctg			913
Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu			
290	295	300	
gag ggg ctg cag gcc atg gtg ggc cag tgt ctg cac agg ctg cag gag			961
Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu			
305	310	315	320
ctg cgt gca gcg gtg gcg gaa cag cca cca aga cca tgt cct gtg ggg			1009
Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly			
325	330	335	
agg ccc ccc gga gcc tcg ccg tcc tgt ggg ggt aga gcg gag cct gca			1057
Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala			
340	345	350	
tgg agc ccc cag ctg ctt gtc tac tcc agc acc cag gag ctg cag acc			1105
Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr			
355	360	365	
ctg gcg gcc ctc aag ctg cga gtg gct gtg ctg gac cag cag atc cac			1153
Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His			
370	375	380	
ttg gaa aag gtc ctg atg gct gaa ctc ctc ccc ctg gta agc gct gca			1201
Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala			
385	390	395	400

cag ccg cag ggg ccg ccc tgg ctg gcc ctg tgc cg^g gct gtg cac agc 1249
Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser
 405 410 415

ctg ctc tgc gag gga gga gca cgt gtc ctt acc atc ctg cg^g gat gaa 1297
Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu
 420 425 430

cct gca gtc tgaggctttc ccatgctgcc ctccgc 1332
Pro Ala Val
 435

<210> 14
<211> 435
<212> PRT
<213> Homo sapiens

<400> 14
Ala Phe Met Leu Pro Ala Gly Cys Ser Arg Arg Leu Val Ala Glu Leu
 1 5 10 15

Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln
 20 25 30

Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly
 35 40 45

Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp
 50 55 60

Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu
 65 70 75 80

Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile
 85 90 95

Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser
 100 105 110

Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro
 115 120 125

Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu
 130 135 140

Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu
 145 150 155 160

Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg
165 170 175

Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro
180 185 190

Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg
195 200 205

Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp
210 215 220

Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala
225 230 235 240

Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro
245 250 255

Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu
260 265 270

Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser
275 280 285

Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu
290 295 300

Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu
305 310 315 320

Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly
325 330 335

Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala
340 345 350

Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr
355 360 365

Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His
370 375 380

Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala
385 390 395 400

Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser
405 410 415

Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu
420 425 430

Pro Ala Val
435

<210> 15
<211> 513
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(510)

<400> 15
atg cag gct caa cag tac cag cag cgt cga aaa ttt gca gct gcc 48
Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
1 5 10 15

ttc ttg gca ttc att ttc ata ctg gca gct gtg gat act gct gaa gca 96
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
20 25 30

ggg aag aaa gag aaa cca gaa aaa aaa gtg aag aag tct gac tgt gga 144
Gly Lys Lys Glu Lys Pro Glu Lys Val Lys Lys Ser Asp Cys Gly
35 40 45

gaa tgg cag tgg agt gtg tgt gtg ccc acc agt gga gac tgt ggg ctg 192
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50 55 60

ggc aca cgg gag ggc act cgg act gga gct gag tgc aag caa acc atg 240
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65 70 75 80

aag acc cag aga tgt aag atc ccc tgc aac tgg aag aag caa ttt ggc 288
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85 90 95

gcg gag tgc aaa tac cag ttc cag gcc tgg gga gaa tgt gac ctg aac 336
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100 105 110

aca gcc ctg aag acc aga act gga agt ctg aag cga gcc ctg cac aat 384

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn			
115	120	125	
gcc gaa tgc cag aag act gtc acc atc tcc aag ccc tgt ggc aaa ctg	432		
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu			
130	135	140	
acc aag ccc aaa cct caa ggt acc cta gaa ctt aaa gta aaa aaa aaa	480		
Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys			
145	150	155	160
aaa aaa aaa aaa aat tct gag gag acc ttt tag	513		
Lys Lys Lys Lys Asn Ser Glu Glu Thr Phe			
165	170		
<210> 16			
<211> 170			
<212> PRT			
<213> Homo sapiens			
<400> 16			
Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala			
1	5	10	15
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala			
20	25	30	
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly			
35	40	45	
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu			
50	55	60	
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met			
65	70	75	80
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly			
85	90	95	
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn			
100	105	110	
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn			
115	120	125	
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu			
130	135	140	

Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys
145 150 155 160

Lys Lys Lys Lys Asn Ser Glu Glu Thr Phe
165 170

<210> 17
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (16) . . . (297)

<400> 17
cgaagggctt tcaca atg cta ggt gtg gtc tgg ctg gtg gca gtc atc gta 51
Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
1 5 10

gga tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc 99
Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
15 20 25

cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct 147
Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Trp Thr Ser Pro
30 35 40

gtg cac cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctc 195
Val His Gln Lys Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu
45 50 55 60

ctg cct ctt atg gaa gaa acg agc tgt cat tat gat ggt gac agt 243
Leu Pro Leu Met Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser
65 70 75

ggt ggc tct ctt tgc tgt gtg ctg ggc acc att cca tgt tgt cca tat 291
Gly Gly Ser Leu Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr
80 85 90

gat gat tgaatacagt aattttgaaa aggaatatga tgatgtcaca atcaagatga 347
Asp Asp

tttttgctat cgtgcaaatt attggatttt ccaactccat ctgtaatccc attgtctatg 407

catttatgaa tgaaaacttc aaaaa

432

<210> 18
<211> 94
<212> PRT
<213> Homo sapiens

<400> 18
Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val Gly Ser Pro Met
1 5 10 15

Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe Leu Tyr Glu Lys
20 25 30

Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro Val His Gln Lys
35 40 45

Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu Leu Pro Leu Met
50 55 60

Glu Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser Gly Gly Ser Leu
65 70 75 80

Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr Asp Asp
85 90

<210> 19
<211> 1425
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (31)..(1395)

<400> 19
ctcctgggga gacgcagcca cttgcccgcc atg gat act ccc agg gtc ctg ctc 54
Met Asp Thr Pro Arg Val Leu Leu
1 5

tcg gcc gtc ttc ctc atc agt ttt ctg tgg gat ttg ccc ggt ttc cag 102
Ser Ala Val Phe Leu Ile Ser Phe Leu Trp Asp Leu Pro Gly Phe Gln
10 15 20

cag gct tcc atc tca tcc tcc tgt tcg tcc gcc gag ctg ggt tcc acc 150

Gln	Ala	Ser	Ile	Ser	Ser	Ser	Cys	Ser	Ser	Ala	Glu	Leu	Gly	Ser	Thr		
25																40	
aag	ggc	atg	cga	agc	cgc	aag	gaa	ggc	aag	atg	cag	cgg	gcg	ccg	cgc	198	
Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg		
																45	
45																50	
gac	agt	gac	gcf	ggc	cgg	gag	ggc	cag	gaa	cca	cag	ccg	cgg	cct	cag	246	
Asp	Ser	Asp	Ala	Gly	Arg	Glu	Gly	Gln	Glu	Pro	Gln	Pro	Gln	Pro	Arg		
																60	
60																65	
gac	gaa	ccc	cgg	gct	cag	cag	ccc	cgg	gcf	cag	gag	ccg	cca	ggc	agg	294	
Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg		
																75	
75																80	
ggt	ccg	cgc	gtg	gtg	ccc	cac	gag	tac	atg	ctg	tca	atc	tac	agg	act	342	
Gly	Pro	Arg	Val	Val	Pro	His	Glu	Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr		
																90	
90																95	
tac	tcc	atc	gct	gag	aag	ctg	ggc	atc	aat	gcc	agc	ttt	ttc	cag	tct	390	
Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser		
																105	
105																110	
tcc	aag	tcg	gct	aat	acg	atc	acc	agc	ttt	gta	gac	agg	gga	cta	gac	438	
Ser	Lys	Ser	Ala	Asn	Thr	Ile	Ser	Thr	Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	
																125	
125																130	
gat	ctc	tcg	cac	act	cct	ctc	cgg	aga	cag	aag	tat	ttg	ttt	gat	gtg	486	
Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val		
																140	
140																145	
tcc	atg	ctc	tca	gac	aaa	gaa	gag	ctg	gtg	ggc	gcf	gag	ctg	cgg	ctc	534	
Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	Leu	Val	Gly	Ala	Glu	Leu	Arg	Leu		
																155	
155																160	
ttt	cgc	cag	gcf	ccc	tca	gcf	ccc	tgg	ggg	cca	cca	gcc	ggg	ccg	ctc	582	
Phe	Arg	Gln	Ala	Pro	Ser	Ala	Pro	Trp	Gly	Pro	Pro	Ala	Gly	Pro	Leu		
																170	
170																175	
cac	gtg	cag	ctc	ttc	cct	tgc	ctt	tcg	ccc	cta	ctg	ctg	gac	gcf	ccg	630	
His	Val	Gln	Leu	Phe	Pro	Cys	Leu	Ser	Pro	Leu	Leu	Leu	Asp	Ala	Arg		
																185	
185																190	
acc	ctg	gac	ccg	cag	ggg	gcf	ccg	ccg	gcc	ggc	tgg	gaa	gtc	ttc	gac	678	
Thr	Leu	Asp	Pro	Gln	Gly	Ala	Pro	Pro	Ala	Gly	Trp	Glu	Val	Phe	Asp		
																205	
205																210	
gtg	tgg	cag	ggc	ctg	cgc	cac	cag	ccc	tgg	aag	cag	ctg	tgc	ttg	gag	726	

Val Trp Gln Gly Leu Arg His Gln Pro Trp Lys Gln Leu Cys Leu Glu			
220	225	230	
ctg cgg gcc gca tgg ggc gag ctg gac gcc ggg gag gcc gag gcg cgc			774
Leu Arg Ala Ala Trp Gly Glu Leu Asp Ala Gly Glu Ala Glu Ala Arg			
235	240	245	
gcg cgg gga ccc cag caa ccg ccg ccc gac ctg cgg agt ctg ggc			822
Ala Arg Gly Pro Gln Gln Pro Pro Pro Asp Leu Arg Ser Leu Gly			
250	255	260	
ttc ggc cgg agg gtg cgg cct ccc cag gag cgg gcc ctg ctg gtg gta			870
Phe Gly Arg Arg Val Arg Pro Pro Gln Glu Arg Ala Leu Leu Val Val			
265	270	275	280
ttc acc aga tcc cag cgc aag aac ctg ttc gca gag atg cgc gag cag			918
Phe Thr Arg Ser Gln Arg Lys Asn Leu Phe Ala Glu Met Arg Glu Gln			
285	290	295	
ctg ggc tcg gcc gag gct gcg ggc ccg ggc gcg ggc gcc gag ggg tcg			966
Leu Gly Ser Ala Glu Ala Ala Gly Pro Gly Ala Gly Ala Glu Gly Ser			
300	305	310	
tgg ccg ccg tcg ggc gcc ccg gat gcc agg cct tgg ctg ccc tcg			1014
Trp Pro Pro Pro Ser Gly Ala Pro Asp Ala Arg Pro Trp Leu Pro Ser			
315	320	325	
ccc ggc cgc ccg ccg cgc acg gcc ttc gcc agt cgc cat ggc aag			1062
Pro Gly Arg Arg Arg Arg Arg Thr Ala Phe Ala Ser Arg His Gly Lys			
330	335	340	
cgg cac ggc aag aag tcc agg cta cgc tgc agc aag aag ccc ctg cac			1110
Arg His Gly Lys Ser Arg Leu Arg Cys Ser Lys Lys Pro Leu His			
345	350	355	360
gtg aac ttc aag gag ctg ggc tgg gac gac tgg att atc gcg ccc ctg			1158
Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp Ile Ile Ala Pro Leu			
365	370	375	
gag tac gag gcc tat cac tgc gag ggt gta tgc gac ttc ccg ctg cgc			1206
Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys Asp Phe Pro Leu Arg			
380	385	390	
tcg cac ctg gag ccc acc aac cac gcc atc atc cag acg ctg atg aac			1254
Ser His Leu Glu Pro Thr Asn His Ala Ile Ile Gln Thr Leu Met Asn			
395	400	405	
tcc atg gac ccc ggc tcc acc ccg ccc agc tgc tgc gtg ccc acc aaa			1302

Ser	Met	Asp	Pro	Gly	Ser	Thr	Pro	Pro	Ser	Cys	Cys	Val	Pro	Thr	Lys	
410					415							420				
ttg act ccc atc agc att cta tac atc gac gcg ggc aat aat gtg gtc 1350																
Leu	Thr	Pro	Ile	Ser	Ile	Leu	Tyr	Ile	Asp	Ala	Gly	Asn	Asn	Val	Val	
425					430							435			440	
tac	aag	cag	tac	gag	gac	atg	gtg	gtg	gag	tcg	tgc	ggc	tgc	agg		1395
Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg		
						445				450				455		
tagcggtgcc tttcccgccg cttggcccg 1425																
<210> 20																
<211> 455																
<212> PRT																
<213> Homo sapiens																
<400> 20																
Met	Asp	Thr	Pro	Arg	Val	Leu	Leu	Ser	Ala	Val	Phe	Leu	Ile	Ser	Phe	
1					5					10				15		
Leu	Trp	Asp	Leu	Pro	Gly	Phe	Gln	Gln	Ala	Ser	Ile	Ser	Ser	Ser	Cys	
						20				25			30			
Ser	Ser	Ala	Glu	Leu	Gly	Ser	Thr	Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	
						35				40			45			
Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg	Asp	Ser	Asp	Ala	Gly	Arg	Glu	Gly	
						50				55			60			
Gln	Glu	Pro	Gln	Pro	Arg	Pro	Gln	Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	
						65				70			75		80	
Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg	Gly	Pro	Arg	Val	Val	Pro	His	Glu	
						85				90			95			
Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr	Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	
						100				105			110			
Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser	Ser	Lys	Ser	Ala	Asn	Thr	Ile	Thr	
						115				120			125			
Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	
						130				135			140			
Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val	Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	

145	150	155	160
Leu Val Gly Ala Glu Leu Arg Leu Phe Arg Gln Ala Pro Ser Ala Pro			
165	170		175
Trp Gly Pro Pro Ala Gly Pro Leu His Val Gln Leu Phe Pro Cys Leu			
180	185		190
Ser Pro Leu Leu Asp Ala Arg Thr Leu Asp Pro Gln Gly Ala Pro			
195	200		205
Pro Ala Gly Trp Glu Val Phe Asp Val Trp Gln Gly Leu Arg His Gln			
210	215		220
Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala Ala Trp Gly Glu Leu			
225	230		240
Asp Ala Gly Glu Ala Glu Ala Arg Ala Arg Gly Pro Gln Gln Pro Pro			
245	250		255
Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly Arg Arg Val Arg Pro Pro			
260	265		270
Gln Glu Arg Ala Leu Leu Val Val Phe Thr Arg Ser Gln Arg Lys Asn			
275	280		285
Leu Phe Ala Glu Met Arg Glu Gln Leu Gly Ser Ala Glu Ala Ala Gly			
290	295		300
Pro Gly Ala Gly Ala Glu Gly Ser Trp Pro Pro Pro Ser Gly Ala Pro			
305	310		320
Asp Ala Arg Pro Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Arg Thr			
325	330		335
Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu			
340	345		350
Arg Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp			
355	360		365
Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu			
370	375		380
Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His			
385	390		400
Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro			

405

410

415

Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr
420 425 430

Ile Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
435 440 445

Val Glu Ser Cys Gly Cys Arg
450 455

<210> 21
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 21

cgatgactc cggagaagg gggccctca cccacatgt aagagccct tctggccac 60
ccagatccat ctccgcactg cttgggtctc tgagtttcag gtcggccctg agaggctggg 120
tggccctgga ccctgccagc ctggggcttg ggctttgtc cccttggggc cttgagtgtg 180
gccagggctc tggcgattgt gtggtgacag aagccatgtc tgcaacgcct gccatccgca 240
gacgtgaatg agtgtgcaga gaaccctggc gtctgcacta acggcgtctg tgtcaacacc 300
gatggatcct tccgctgtga gtgtccctt ggctacagcc tggacttcac tggcatcaac 360
tgtgtggaca cagacgagtg ctctgtcggc cacccctgtg ggcaaggac atgcaccaat 420
gtcatcgagg gcttcgaatg tgcctgtgt gacggcttt agcctggcct catgtatgacc 480
tgcgaggaca tcgacgaatg ctccctgaac ccgctgtct gtgccttcgg ctgcacaaat 540
accgagggct cctacctgtg cacctgtcca gcccgtaca ccctgcgggaa ggacggggcc 600
atgtgtcgag atgtggacga gtgtgcagat ggtcagcagg actgccacgc ccggggcatg 660
gagtgcaga acctcatcggt taccttcggc tgcgtctgtc ccccaaggcat gcggccccctg 720
cctggctctg gggagggctg cacagatgac aatgaatgcc acgctcagcc tgacctctgt 780
gtcaacggcc gctgtgtcaa caccgcggg agcttcggg ggcactgtg tgaggattc 840
cagcccagcc ccacccttac cgagtgcac gacatccggc agggggccctg ctttgcggag 900
gtgctgcaga ccatgtgccg gtctctgtcc agcagcagtg aggctgtcac caggccgag 960
tgctgctgtg ggggtggccg gggctggggg ccccgctgca agctctgtcc cctggccggc 1020
acctctgcct acaggaagct gtgcggccat ggctcaggct acactgtca gggccgagat 1080
gttagatgaat gcccgtatgt tgctcacctg tgcgtcatg gggagggtcat caacagcctt 1140
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ctggatatgg atgagtgccg ccagggtcccc aagccatgtc ctttcctctg caaaaacacg 1260
aaggcagtt tcctgtgcag ctgtccccga ggctacctgc tggaggaggaa tggcaggacc 1320
tgc当地 accatggc tggacgaatg caccccccgg cagcacaact gtcagttcct ctgtgtcaac 1380
actgtggccg cttcacctg ccgctgtcca cccggctca cccagcacca ccaggcctgc 1440
ttcgacaatg atgagtgctc agcccagct ggcccatgtg gtgcggccacg gcaactgcac 1500
aacaccccccgg gcagcttccg ctgtgaatgc caccaaggct tcaccctgtt cagctcaggc 1560
catggctgtg aagatgtgaa tgaatgtgat gggcccccacc gctgcacca tggctgtcag 1620
aaccagctag ggggctaccg ctgcagctgc ccccaagggtt tcacccagca ctcccagtgg 1680
gcccagtgtg tgggtgagtg aaaagggtg ggaagaagct gggccctcca ccagaatctg 1740

ctcagagcag gcgactaaca gacgccaccc tgcaagatga tgtgacaagg acaattatct 1800
aaagattgaa caggccagcc cagaagatga gaatgagtgt gccctgtcgc cc 1852

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 390

<400> 22
accaatgtca tcggaggctt 20

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
Ag 390

<400> 23
gatgtcctcg caggtcatca t 21

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer
Ag390

<400> 24
tcaaagccgt cagcacaggc aca 23

<210> 25
<211> 379
<212> DNA
<213> Homo sapiens

<400> 25
ggagggcctg tgattctact gcagggcaggc acccccccaca acctcacatg ccgggccttc 60
aatgcgaagc ctgctgccac catcatctgg ttccgggacg ggacgcagca ggagggcgct 120
gtggccagca cgaaattgct gaaggatggg aagagggaga ccaccgtgag ccaactgctt 180
attaacccca cggacctgga catagggcgt gtcttcactt gccgaagcat gaacaagcc 240
atcccttagtg gcaaggagac ttccatcgag ctggatgtgc accaccctcc tacagtgacc 300
ctgtccattg agccacagac gggcaggag ggtgagcgtg ttgtcttac ctgccaggcc 360
acagccaacc ccgagatct 379

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 271

<400> 26
acctggacat agggcgtgtc t 21

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
Ag 271

<400> 27
tcgatgaaag tctccttgcc 20

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer Ag
271

<400> 28
cgaagcatga acgaagccat ccctag 26

<210> 29
<211> 234
<212> DNA
<213> Homo sapiens

<400> 29
tccaatctca catgcacgca cagccggcct gaggcggtcca gcatcaggcc ctctggacac 60
tcacagcgga aagaccaggc agtgttgacg caacgcccgt tgggacagac tccccggaaag 120
gactcacact cgttcacatc atcgcagggt acacccgtca tccgggcaaa gccccgggca 180
caggcagggt cgatctcgca gcgttcgcag gggctccccc aggctgcccc gagg 234

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 72

<400> 30
cgaaaaagacc cagcagtgtt 20

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
Ag 72

<400> 31
atgatgtgaa cgagtgtgag tcctt 25

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer Ag
72

<400> 32
cgcccgttgg gacagactcc c

21

<210> 33
<211> 439
<212> DNA
<213> Homo sapiens

<400> 33
tcacggaaat aagcctgggc ccgtcccttt gatttccaac aagatctgca accacaggga 60
cgtgtacggt ggcacatcatct cccccctccat gctctgcgcg ggctacctga cgggtggcgt 120
ggacagctgc cagggggaca gcggggggcc cctggtgtgt caagagagga ggctgtggaa 180
gttagtggga ggcaccagct ttggcatcggt ctgcgcagag gtgaacaaggc ctgggtgtta 240
caccgtgtca cctccttcct ggactggatc cacgagcaga tggagagaga cctaaaaacc 300
tgaagaggaa ggggataagt agccacctga gttcctgagg tgatgaagac agcccgatcc 360
tcccctggac tcccgtgttag gaacctgcac acgagcagac acccttggag ctctgagttc 420
cggcaccagt agcaggccc 439

<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 248

<400> 34
tttccaacaa gatctgcaac ca

22

<210> 35
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
Ag 248

<400> 35
aggttagcccg cgcaagag

17

<210> 36
<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer Ag
248

<400> 36

cgtgtacggt ggcatcatct cccc

24

<210> 37

<211> 410

<212> DNA

<213> Homo sapiens

<400> 37

tgtcattgtc cttaaaccta ttatatttt tcataactctg tgaaaacaaa tcagttgccg 60
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cttattgcaa ctcagactgc aattgtgatg aaagtcagtg ggaaccagtc tgtggaaaca 180
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agcatacagt gtttataac ttagttgtg tggaagtaac tggctccag aacagaaatt 300
actcagcgca cttgggtgaa tgcccaagag ataatacttg tacaaggaaa ttttcatct 360
atgttcaat tcaagtcata aactcttgc tctctgcaac aggaggtacc 410

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward Primer
Ag 287

<400> 38

aactcagact gcaattgtga tgaaa

25

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Primer
Ag 287

<400> 39
ctagacaagg tgacaggtaa gttattcc 28

<210> 40
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer Ag
287

<400> 40
ttgttcccac agactggttc ccactgt 27

<210> 41
<211> 322
<212> DNA
<213> Homo sapiens

<400> 41
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ggcccgatga ggaagaggca gagttgcggg gcgaacacac gtcacagag aagttgtct 180
gcctggatga ctccttggc catgactgca gcttgacctg tcatgactgc aggaacggag 240
ggacctgcct cctggcctg gatggctgtg attgccccga ggggtggact ggggttattt 300
gcaatgagat ttgtccctcg ga 322

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 252

<400> 42
gagctgccgc aactcttcc 19

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Primer
Ag 252

<400> 43

gacaaaacttc tctgtgagcg tgtg

24

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Primer Ag
252

<400> 44

cgcgaactctg cctcttcctc atcgg

25

<210> 45

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 45

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gctgcatgcc tgggaaccaa ctgggaccgg ggctttaag ccacctccag ggccagaaac 180
taatggagag gaccccttc cagcatgcac acccagtcca caagacctca aagagttgga 240
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agagagagac aaggccccca gcctgaaatc taggtccatt gtcaccttt ctggcacgac 360
agccctccgccc ccaccgcatt ccccaaggcca agctggtggc catgcttcag acacgagacc 420
caccaagggc ctccggcaga ccacgggtgcc tgccaaaggc caccctgagc gccggctgct 480
gtcagtgggg gatggacccc gtgttggat gggagccgaa acccccaggc ctggggcggt 540
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gctgccctcg gc 1332

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ab16

<400> 46
ggcattcagg aaagcagctt 20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
Ab16

<400> 47
gcatccgtgg aatcactgg 20

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer
Ab16

<400> 48
tgggcccagc tcagttccac aca 23

<210> 49
<211> 513
<212> DNA
<213> Homo sapiens

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aaagtgaaga agtctgactg tggagaatgg cagtgagtg tgtgtgtgcc caccagtgg 180
gactgtgggc tggcacacg ggagggcact cggactggag ctgagtgcaa gcaaaccatg 240
aagaccaga gatgtaaatcccctgcaac tggaagaagc aatttggcgcc ggagtgc当地 300
taccagttcc aggcctgggg agaatgtgac ctgaacacag ccctgaagac cagaactgg 360
agtctgaagc gagccctgca caatgccgaa tgccagaaga ctgtcaccat ctccaagccc 420
tgtggcaaac tgaccaagcc caaacctcaa ggtaccctag aacttaaagt aaaaaaaaaa 480
aaaaaaaaaaa aaaattctga ggagacctt tag 513

<210> 50
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 177

<400> 50
ccctgcacaa tgccgaat 18

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 177

<400> 51
tgagggtttgg gcttggtcag 20

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Ag 177

<400> 52
caccatctcc aagccctgtg gcaa

24

<210> 53
<211> 432
<212> DNA
<213> Homo sapiens

<400> 53
ttttgaagt tttcattcat aaatgcata gcaatggat tacagatgga gttggaaaat 60
ccaataattt gcacgatagc aaaaatcatc ttgattgtga catcatcata ttccctttca 120
aaattactgt attcaatcat catatggaca acatggaatg gtgcccagca cacagcaaag 180
agagccacca ctgtcaccat cataatgaca gtcgttct tcttcataa gaggcaggag 240
gaagaggatg acaaggatga aggtggtga gatcttctgg tgcacagggc tggccactc 300
ttctaaggcg cagatgtt ctttcata taggaagtca tatttgatct caagttgtt 360
cacgtgccac atgggtgatc ctacgatgac tgccaccagc cagaccacac ctagcattgt 420
gaaagccctt cg 432

<210> 54
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
GPCR 13

<400> 54
atggaatggt gcccagca 18

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse Primer
GPCR 13

<400> 55
tggaagaaga aacgagctgt ca 22

<210> 56
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe Primer
 GPCR 13

<400> 56
cagcaaaagag agccaccact gtcacca

27

<210> 57
<211> 102
<212> DNA
<213> *Homo sapiens*

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<220>
<221> misc_feature
<222> (1)..(2)
<223> Wherein n is a or t or g or c.
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<220>
<221> misc_feature
<222> (101)..(102)
<223> Wherein n is t or a or g or c.
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<400> 57
nngacttact ccatcgctga gaagctggc atcaatgcc a gcttttcca gtcttccaag 60
tcqqqctaata cqatcaccaq ctttqtaqac aqqqqactaa nn 102

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward Primer
Aq 191

<400> 58

24

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Reverse Primer
      Ag 191

<400> 59
gctggtgatc gtattagccg a                                21

<210> 60
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Probe Primer Ag
      191

<400> 60
catcaatgcc agcttttcc agtcttcc                                28

<210> 61
<211> 238
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (104)
<223> Wherein n is t or a or g or c.

<400> 61
tcaaacactga tggatcttc cgatgtgagt gtccaatggg ctacaacctg gattacactg 60
gagtccggtg tggacact gacgagtgct ccattggcaa ccntgcggg aacgggacat 120
gcaccaacgt gatcggtgc ttcaatgca cctgaaacga aggcttgag ccggggccca 180
tcatgaaactg cgaagacatc aacgagtgcc cccagaaccc gctgcttgt gcttccg    238

<210> 62
<211> 197
<212> DNA
<213> Mus musculus

<400> 62
aagccatgca acttcatctg caagaacacc aaggcgagtt accagtgctc ctgcccacgg 60
gggtacgtcc tgcaggagga cggaaagacg tgcaaagacc tcgacgaatg tcaaacaaa 120
cagcacaact gccaggcct ctgtgtcaac accctggggg gattcacctg taaatgtccg 180

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<210> 63
<211> 492
<212> PRT
<213> Homo sapiens

<400> 63

Met	Ala	Leu	Asn	Ser	Gly	Ser	Pro	Pro	Ala	Ile	Gly	Pro	Tyr	Tyr	Glu	
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Asn	His	Gly	Tyr	Gln	Pro	Glu	Asn	Pro	Tyr	Pro	Ala	Gln	Pro	Thr	Val	
																30

Val	Pro	Thr	Val	Tyr	Glu	Val	His	Pro	Ala	Gln	Tyr	Tyr	Pro	Ser	Pro	
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Val	Pro	Gln	Tyr	Ala	Pro	Arg	Val	Leu	Thr	Gln	Ala	Ser	Asn	Pro	Val	
																60

Val	Cys	Thr	Gln	Pro	Lys	Ser	Pro	Ser	Gly	Thr	Val	Cys	Thr	Ser	Lys	
																80

Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val	
																95

Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys	
																110

Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	
																125

Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	
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Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met	
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Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp	
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Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn	
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Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	
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Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220

Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240

Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270

Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
275 280 285

Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
290 295 300

Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305 310 315 320

Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
325 330 335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
340 345 350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385 390 395 400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
405 410 415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asp Gly
485 490

<210> 64

<211> 2656

<212> DNA

<213> Homo sapiens

<400> 64

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<210> 65

<211> 1011

<212> PRT

<213> Drosophila melanogaster

<400> 65

Met Ala Leu Arg Gln Ser Ala Lys Asp Val Ala Lys Ser Asn Cys Val
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20 25 30

Ala Leu Val Asp Ser Ser Thr Ala Gln Val Asp Thr Thr Ile Ser Gln
35 40 45

Gln Glu Ser Gln Ser Val Val Leu Pro Cys Pro Val Asp Ala Glu Lys
50 55 60

Cys Gly Lys Leu His Ser Leu Asn Trp Phe Lys Gly Asp Asp Arg Ile
65 70 75 80

Ala Ala Met Leu Leu Gly Asp Ser Asn Val Thr Ser Val Asn Lys Glu
85 90 95

Phe Asp Glu Arg Val Thr Val Glu Gln Asn Pro Tyr Arg Leu Val Ile
100 105 110

Lys Asp Leu Lys Ile Ala Asp Glu Asp Ile Tyr Leu Cys Asp Thr Thr
115 120 125

Phe Phe Ile Pro Glu Glu Thr Cys Asp Asn Phe Asn Gly Tyr Arg Ile
130 135 140

Glu Leu Arg Val Leu Val Pro Pro Thr Glu Val Val Ile Leu Asp Ala
145 150 155 160

Lys Gly Asp Arg Ile Lys Asn Gly Ser Val Val Gly Pro Met Gln Glu
165 170 175

Arg Gln Ser Leu Lys Ala Thr Cys Thr Val Arg Asn Thr Arg Pro Gln
180 185 190

Pro Glu Val Ser Trp Phe Arg Gly Thr Lys Arg Leu Thr Thr Tyr Ser
195 200 205

Pro Thr His Asp Leu Val Asp Gly Leu Tyr Thr Ser Thr Leu Glu Leu
210 215 220

Asp Trp Thr Leu Ser Arg Glu Asp Leu Ala Gln Asp Ile Glu Cys Arg
225 230 235 240

Val Lys Ser Ala Ala Ile Gln Asn Val Thr Val Thr Lys Phe Ser Val
245 250 255

Asp Leu Gln Val Arg Pro Thr Ser Ile Asp Ile Asn Gly Val Lys His
260 265 270

His Thr Val Gln Gly Ser Lys Val Val Leu Thr Cys Asp Ile His Gly
275 280 285

Ala Arg Pro Ala Val Asn Leu Thr Trp Tyr Asn Thr Thr Thr Ile Ile
290 295 300

Ser Ser Gly Glu Asn Glu Ile Thr Glu Val Arg Ser Lys Ser Leu Glu
305 310 315 320

Lys Ser Asp Gly Thr Phe His Thr Gln Ser Glu Leu Ile Phe Asn Ala
325 330 335

Thr Arg Phe Glu Asn Asp Arg Val Phe Arg Cys Glu Ala Glu Asn Ile
340 345 350

Val Leu Gln Ile Asn Arg Glu Lys Pro Ile Ser Ser Ala Leu Thr Leu
355 360 365

Glu Val Leu Tyr Pro Pro Val Val Lys Val Ser Pro Ser Ala Ile Thr
370 375 380

Ala Asn Thr Ser Glu Ile Val Leu Leu Asn Cys Glu Tyr Phe Ala Asn
385 390 395 400

Pro Ala Ser Leu Thr Gln Val Glu Trp Tyr Arg Asn Asp Ile Leu Val
405 410 415

Asn Val Asn Asp Thr Thr His Tyr Lys Gly Gly Asn Ser Glu Asn Val
420 425 430

Ala Leu Val Ile Lys Ser Thr Glu Lys Glu Asp Ile Gly Asn Tyr Ser
435 440 445

Cys Gln Leu Ser Asn Asn Ile Gly Lys Gly Thr Ser Asp Gln Lys Ile
450 455 460

Asn Leu Asp Val Gln Tyr Ala Pro Thr Val Glu Ile Leu Met Ile Pro
465 470 475 480

Glu Gly Pro Val Lys Glu Ser Asp Glu Ser Asn Val Thr Leu Phe Cys
485 490 495

Asn Val Leu Asp Ala Asn Pro Ser Val Leu Thr Lys Val Arg Trp Tyr
500 505 510

Ala Asn Ser Thr Leu Leu Lys Glu Leu Pro Asp Cys Glu Glu Thr Arg
515 520 525

Glu Asp Leu Cys His Ile Asp Pro Ser Lys Leu Leu Leu Glu Ser Ile
530 535 540

Gly Arg Gly Phe Phe Tyr Asn Tyr Ser Cys Glu Gly Phe Asn Ala Ala
545 550 555 560

Gly Trp Gly Pro Arg Ser Glu Asp Lys Glu Leu Leu Val His Tyr Glu
565 570 575

Pro Gly Pro Ala Ala Leu Ser His Phe Pro Leu Val Ala Val Lys Lys
580 585 590

Lys Ser Val Thr Phe Ser Cys Ser Val Asp Asp Pro Gly Phe Pro Glu
595 600 605

Ser Asn Arg Phe Arg Trp Leu Arg Gly Arg Gly Pro Leu Gln Asp
610 615 620

Ile Val Thr Lys Asp Trp Thr Val Glu Pro Val Gly Leu Asp Ser Arg
625 630 635 640

Thr Asn Tyr Ser Cys Tyr Ala Tyr Asn Glu Gly Gly Lys Gly Val Met
645 650 655

Ala Thr Val Asn Leu Glu Val His Ala Pro Pro Phe Phe Ile Lys Asn
660 665 670

Leu Pro Pro Tyr Thr Gly Ile Leu His Ser Ser Pro Asn Ala Thr Leu
675 680 685

Thr Cys Arg Ile Glu Cys Val Pro Arg Cys Asp Ile Ser Trp Gln Lys
690 695 700

Asp Gly Val Pro Ile Glu Arg Asn Asp Ser Arg Tyr Phe Ile Lys Glu
705 710 715 720

Asn Thr Trp Met Pro Pro Pro Gln Arg Glu Ile Leu Lys Ser Met Leu
725 730 735

Ser Val Leu His Phe Asn Met Pro Asn Trp Pro Asp Ser Lys Phe Asn
740 745 750

Ile Glu Ala Asp Asn Ala Asn Tyr Ser Cys Val Ser Thr Gly Asn Ile
755 760 765

Val Gly Gly Ser Ile Arg Ser Arg Thr Tyr Tyr Phe Gly Ile Glu Ala
770 775 780

Pro Glu Asn Thr Thr Val Ser Glu Asn Ile Val Tyr Val Gln Glu Asp
785 790 795 800

Thr Ile Pro Gly Arg Val Ile Cys Lys Ser Arg Ala Asn Pro Glu Pro
805 810 815

Ser Tyr Lys Trp Ile Phe Lys Asn Glu Thr Ile Ala Asn Gly Asn Ala
820 825 830

Leu Ile Ile Asn Thr Ala Met Asn Arg Asn Asp Asp Gly Thr Tyr Thr
835 840 845

Cys Leu Ala Tyr Asn Lys His Gly Ser Ser Ile Ala Lys Thr Val Ile
850 855 860

Lys Val Gln Phe Lys Pro Arg Cys Glu Ile Glu Arg Gln Glu Ile Asp
865 870 875 880

Asp Gln Asp Thr Leu Ile Cys Thr Ala Tyr Gly Asn Pro Ile Glu Ala
885 890 895

Asp Phe Ser Trp Ser Ile Lys Thr Glu Asn Glu Thr Asp Glu Asn Leu
900 905 910

Gly Ser Gly Lys Lys Glu Asn Ser Val Glu Lys Ser Phe Tyr Ile Leu
915 920 925

Gln Thr Asp Tyr Ala Ile Ser Arg Thr Tyr Arg Cys Val Ala Asn Asn
930 935 940

Thr Val Gly Tyr Gly Pro Phe Cys Glu Ile Glu Val Ala Glu Gln Leu
945 950 955 960

Ala Trp Trp Gln Leu Trp Glu Lys Asn Thr Leu Ile Ile Leu Val Ala
965 970 975

Ala Ile Leu Gly Leu Leu Leu Thr Val Ile Val Ile Cys Cys Ile Ile
980 985 990

Ile Cys Ile Cys Arg Pro Val Gly Ala Arg Ile Asn Tyr Thr Thr Ser
995 1000 1005

Arg Leu His
1010

<210> 66

<211> 862

<212> PRT

<213> Mus musculus

<400> 66

Met Arg Val His Tyr Leu Trp Leu Leu Leu Ile Leu Gly His Ala Ala
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Ser Ala Gln Tyr Ser Ser Ala Asn Asp Trp Thr Val Asp His Pro Gln
20 25 30

Thr Leu Phe Ala Trp Glu Gly Ala Cys Ile Arg Ile Pro Cys Lys Tyr
35 40 45

Lys Thr Pro Leu Pro Lys Ala Arg Leu Asp Asn Ile Leu Leu Phe Gln
50 55 60

Asn Tyr Glu Phe Asp Lys Ala Thr Lys Lys Phe Lys Gly Thr Val Leu
65 70 75 80

Tyr Asn Lys Ala Glu Pro Glu Leu Tyr Pro Pro Lys Gln Arg Arg Val
85 90 95

Thr Phe Leu Gly Asn Ser Ile Asp Asn Cys Thr Leu Lys Ile His Pro
100 105 110

Ile Arg Ala Asn Asp Ser Gly Asn Leu Gly Leu Arg Met Thr Ala Gly
115 120 125

Thr Glu Arg Trp Met Glu Pro Ile His Leu Asn Val Ser Glu Lys Pro
130 135 140

Phe Gln Pro Tyr Ile Gln Met Pro Ser Glu Ile Arg Glu Ser Gln Ser
145 150 155 160

Val Thr Leu Thr Cys Gly Leu Asn Phe Ser Cys Phe Glu Tyr Asp Ile
165 170 175

Leu Leu Gln Trp Phe Leu Glu Asp Ser Lys Ile Thr Ser Val Thr Pro
180 185 190

Ser Val Thr Ser Ile Thr Ser Ser Val Thr Ser Ser Ile Lys Asn Val
195 200 205

Tyr Thr Glu Ser Lys Leu Thr Phe Gln Pro Lys Trp Thr Asp His Gly
210 215 220

Lys Ser Val Lys Cys Gln Val Gln His Ser Ser Glu Val Leu Ser Glu
225 230 235 240

Arg Thr Val Arg Leu Asp Val Lys Tyr Thr Pro Lys Leu Glu Ile Lys
245 250 255

Val Asn Pro Thr Glu Val Glu Lys Asn Asn Ser Val Thr Met Thr Cys
260 265 270

Arg Val Asn Ser Ser Asn Pro Lys Leu Arg Thr Val Ala Val Ser Trp
275 280 285

Phe Lys Asp Gly Arg Pro Leu Glu Asp Gln Glu Leu Glu Gln Glu Gln
290 295 300

Gln Met Ser Lys Leu Ile Leu His Ser Val Thr Lys Asp Met Arg Gly
305 310 315 320

Lys Tyr Arg Cys Gln Ala Ser Asn Asp Ile Gly Pro Gly Glu Ser Glu
325 330 335

Glu Val Glu Leu Thr Val His Tyr Ala Pro Glu Pro Ser Arg Val His
340 345 350

Ile Tyr Pro Ser Pro Ala Glu Glu Gly Gln Ser Val Glu Leu Ile Cys
355 360 365

Glu Ser Leu Ala Ser Pro Ser Ala Thr Asn Tyr Thr Trp Tyr His Asn
370 375 380

Arg Lys Pro Ile Pro Gly Asp Thr Gln Glu Lys Leu Arg Ile Pro Lys
385 390 395 400

Val Ser Pro Trp His Ala Gly Asn Tyr Ser Cys Leu Ala Glu Asn Arg
405 410 415

Leu Gly His Gly Lys Ile Asp Gln Glu Ala Lys Leu Asp Val His Tyr
420 425 430

Ala Pro Lys Ala Val Thr Thr Val Ile Gln Ser Phe Thr Pro Ile Leu
435 440 445

Glu Gly Asp Ser Val Thr Leu Val Cys Arg Tyr Asn Ser Ser Asn Pro
450 455 460

Asp Val Thr Ser Tyr Arg Trp Asn Pro Gln Gly Ser Gly Ser Val Leu
465 470 475 480

Lys Pro Gly Val Leu Arg Ile Gln Lys Val Thr Trp Asp Ser Met Pro
485 490 495

Val Ser Cys Ala Ala Cys Asn His Lys Cys Ser Trp Ala Leu Pro Val
500 505 510

Ile Leu Asn Val His Tyr Ala Pro Arg Asp Val Lys Val Leu Lys Val
515 520 525

Ser Pro Ala Ser Glu Ile Arg Ala Gly Gln Arg Val Leu Leu Gln Cys
530 535 540

Asp Phe Ala Glu Ser Asn Pro Ala Glu Val Arg Phe Phe Trp Lys Lys
545 550 555 560

Asn Gly Ser Leu Val Gln Glu Gly Arg Tyr Leu Ser Phe Gly Ser Val
565 570 575

Ser Pro Glu Asp Ser Gly Asn Tyr Asn Cys Met Val Asn Asn Ser Ile
580 585 590

Gly Glu Thr Leu Ser Gln Ala Trp Asn Leu Gln Val Leu Tyr Ala Pro
595 600 605

Arg Arg Leu Arg Val Ser Ile Ser Pro Gly Asp His Val Met Glu Gly
610 615 620

Lys Lys Ala Thr Leu Ser Cys Glu Ser Asp Ala Asn Pro Pro Ile Ser
625 630 635 640

Gln Tyr Thr Trp Phe Asp Ser Ser Gly Gln Asp Leu His Ser Ser Gly
 645 650 655

 Gln Lys Leu Arg Leu Glu Pro Leu Glu Val Gln His Thr Gly Ser Tyr
 660 665 670

 Arg Cys Lys Gly Thr Asn Gly Ile Gly Thr Gly Glu Ser Pro Pro Ser
 675 680 685

 Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Lys Arg Val Ala
 690 695 700

 Leu Gly Leu Gly Phe Cys Leu Thr Ile Cys Ile Leu Ala Ile Trp Gly
 705 710 715 720

 Met Lys Ile Gln Lys Lys Trp Lys Gln Asn Arg Ser Gln Gln Gly Leu
 725 730 735

 Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Ala
 740 745 750

 Arg Arg Thr Pro Leu Ser Glu Gly Pro Gln Ser Gln Gly Cys Tyr Asn
 755 760 765

 Pro Ala Met Asp Asp Thr Val Ser Tyr Ala Ile Leu Arg Phe Pro Glu
 770 775 780

 Ser Asp Met His Asn Ala Gly Asp Ala Gly Thr Pro Ala Thr Gln Ala
 785 790 795 800

 Pro Pro Pro Asn Asn Ser Asp Ser Val Thr Tyr Ser Val Ile Gln Lys
 805 810 815

 Arg Pro Met Gly Asp Tyr Glu Asn Val Asn Pro Ser Cys Pro Glu Asp
 820 825 830

 Glu Ser Ile His Tyr Ser Glu Leu Val Gln Phe Gly Ala Gly Lys Arg
 835 840 845

 Pro Gln Ala Lys Glu Asp Val Asp Tyr Val Thr Leu Lys His
 850 855 860

<210> 67
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<400> 67

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agggacccccc ctgcctcgatg ccccatgtatg cggcccacat ggcgcctccg gcctctgccc 180
ccctctcccc acagatatcg acgagtgtcg catctctccat gacctctgcg gccagggcac 240
ctgtgtcaac acgccccca gctttgatg cgagtgtttt cccggctacg agagtggctt 300
catgctgtatg aagaactgca tgggtcggtg actgcccggc aggggtgtgg tggcgccct 360
gggcaggggag ggcattgagg agagggaggg tggggacggc tggtgctgtg tggacgtgga 420
tggagggggc aggaggaggg aggagctgtatg aattagctga ggtacagtga gtctgggctc 480
catgaggccct cgtcccttagg agagagacct ggggcctgag acctgggggt ggccggcaca 540
ctgggggtgtg gtctcccagg gagggtgtgt agcttggta gaggacagg accctcagag 600
aagcctggga aatactgccc gttatgaggc ctctcgatcc catcattgac ttcgttattc 660
atttgatgag catttcacat gcatcctctg agctagaggc actgcaggaa gctctagctc 720
cagggagccc tcctttcttg gagctcacatg cctaacaaggaa agacagacat gaataacatg 780
aatcgctgaa gaaatcaaaa actgggctgg gtgcagtggc cctcgctgt aatcccagca 840
tttgagagg ctgaggcagt aggattgtt gagtccagga gttcgaggcc agcctgggca 900
acataacaag accctgtcac tacaaagttt tttaaaaattt agctaggcat ggtggcgcgt 960
gctactcgaa aggctgagga gggaggatcc ctgagccca ggaggttgag gctcagtgaa 1020
accataatcg cactttgca ctccagcctg ggtgacagag tgagaccctg tctaaagaaa 1080
aaaggaagga aggaaggaag gaagaggaaa aagccaggca tggtgctca tgcctgtat 1140
cccagcaactt tgggaggctg aggtgggcaag attgcctgag ttcaggagtt tgaaaccagc 1200
ctgggcaaca tggtaaaacc ccgtctctat taaaatacaa aaaattagct gcgtgtggtg 1260
gctgtcacctt gtaggtccag ctactcagga ggctgaggca ggagaattgc ttgaacccag 1320
gaggtggagg ttgcagtgag ccgagatcgc gccactgcac tccagcctgg ggcacagagc 1380
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<210> 68

<211> 2911

<212> PRT

<213> Homo sapiens

<400> 68

Met Gly Arg Arg Arg Arg Leu Cys Leu Gln Leu Tyr Phe Leu Trp Leu

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Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg

35 40 45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg

50 55 60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Gly Gln Gln

65 70 75 80

Asp Val Leu Arg Gly Pro Asn Val Cys Gly Ser Arg Phe His Ser Tyr			
85	90	95	
Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys Ile Val			
100	105	110	
Pro Ile Cys Arg Asn Ser Cys Gly Asp Gly Phe Cys Ser Arg Pro Asn			
115	120	125	
Met Cys Thr Cys Ser Ser Gly Gln Ile Ser Ser Thr Cys Gly Ser Lys			
130	135	140	
Ser Ile Gln Gln Cys Ser Val Arg Cys Met Asn Gly Gly Thr Cys Ala			
145	150	155	160
Asp Asp His Cys Gln Cys Gln Lys Gly Tyr Ile Gly Thr Tyr Cys Gly			
165	170	175	
Gln Pro Val Cys Glu Asn Gly Cys Gln Asn Gly Gly Arg Cys Ile Ala			
180	185	190	
Gln Pro Cys Ala Cys Val Tyr Gly Phe Thr Gly Pro Gln Cys Glu Arg			
195	200	205	
Asp Tyr Arg Thr Gly Pro Cys Phe Thr Gln Val Asn Asn Gln Met Cys			
210	215	220	
Gln Gly Gln Leu Thr Gly Ile Val Cys Thr Lys Thr Leu Cys Cys Ala			
225	230	235	240
Thr Thr Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys Pro Ala Gln			
245	250	255	
Pro Gln Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg Thr Gly Ala			
260	265	270	
Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Ile Cys Gln Gly			
275	280	285	
Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Arg Cys Pro Ala			
290	295	300	
Gly His Lys Gln Ser Glu Thr Thr Gln Lys Cys Glu Asp Ile Asp Glu			
305	310	315	320
Cys Ser Ile Ile Pro Gly Ile Cys Glu Thr Gly Glu Cys Ser Asn Thr			
325	330	335	

Val Gly Ser Tyr Phe Cys Val Cys Pro Arg Gly Tyr Val Thr Ser Thr
340 345 350

Asp Gly Ser Arg Cys Ile Asp Gln Arg Thr Gly Met Cys Phe Ser Gly
355 360 365

Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr Lys
370 375 380

Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr Ile
385 390 395 400

Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu Cys
405 410 415

Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser Arg
420 425 430

Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly Asn
435 440 445

Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly Asn
450 455 460

Gly Phe Ser Pro Gly Val Gly Ala Gly Val Gly Ala Gly Gly Gln
465 470 475 480

Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp Ile
485 490 495

Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro Thr
500 505 510

Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp Ala
515 520 525

Asn Gly Asp Cys Ile Asp Val Asp Glu Cys Thr Ser Asn Pro Cys Thr
530 535 540

Asn Gly Asp Cys Val Asn Thr Pro Gly Ser Tyr Tyr Cys Lys Cys His
545 550 555 560

Ala Gly Phe Gln Arg Thr Pro Thr Lys Gln Ala Cys Ile Asp Ile Asp
565 570 575

Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val Asn
580 585 590

Ser Asp Gly Ser Phe Gln Cys Ile Cys Asn Ala Gly Phe Glu Leu Thr
595 600 605

Thr Asp Gly Lys Asn Cys Val Asp His Asp Glu Cys Thr Thr Thr Asn
610 615 620

Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly Ser Phe Lys Cys
625 630 635 640

Ile Cys Lys Pro Gly Phe Val Leu Ala Pro Asn Gly Arg Tyr Cys Thr
645 650 655

Asp Val Asp Glu Cys Gln Thr Pro Gly Ile Cys Met Asn Gly His Cys
660 665 670

Ile Asn Ser Glu Gly Ser Phe Arg Cys Asp Cys Pro Pro Gly Leu Ala
675 680 685

Val Gly Met Asp Gly Arg Val Cys Val Asp Thr His Met Arg Ser Thr
690 695 700

Cys Tyr Gly Gly Ile Lys Lys Gly Val Cys Val Arg Pro Phe Pro Gly
705 710 715 720

Ala Val Thr Lys Ser Glu Cys Cys Ala Asn Pro Asp Tyr Gly Phe
725 730 735

Gly Glu Pro Cys Gln Pro Cys Pro Ala Lys Asn Ser Ala Glu Phe His
740 745 750

Gly Leu Cys Ser Ser Gly Val Gly Ile Thr Val Asp Gly Arg Asp Ile
755 760 765

Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Ala Asn Gly Ile Cys Glu
770 775 780

Asn Leu Arg Gly Ser Tyr Arg Cys Asn Cys Asn Ser Gly Tyr Glu Pro
785 790 795 800

Asp Ala Ser Gly Arg Asn Cys Ile Asp Ile Asp Glu Cys Leu Val Asn
805 810 815

Arg Leu Leu Cys Asp Asn Gly Leu Cys Arg Asn Thr Pro Gly Ser Tyr
820 825 830

Ser Cys Thr Cys Pro Pro Gly Tyr Val Phe Arg Thr Glu Thr Glu Thr
835 840 845

Cys Glu Asp Ile Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Ala
850 855 860

Cys Arg Asn Asn Leu Gly Ser Phe Asn Cys Glu Cys Ser Pro Gly Ser
865 870 875 880

Lys Leu Ser Ser Thr Gly Leu Ile Cys Ile Asp Ser Leu Lys Gly Thr
885 890 895

Cys Trp Leu Asn Ile Gln Asp Ser Arg Cys Glu Val Asn Ile Asn Gly
900 905 910

Ala Thr Leu Lys Ser Glu Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly
915 920 925

Ser Pro Cys Glu Arg Cys Glu Leu Asp Thr Ala Cys Pro Arg Gly Leu
930 935 940

Ala Arg Ile Lys Gly Val Thr Cys Glu Asp Val Asn Glu Cys Glu Val
945 950 955 960

Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Ser Lys Gly Ser
965 970 975

Phe His Cys Glu Cys Pro Glu Gly Leu Thr Leu Asp Gly Thr Gly Arg
980 985 990

Val Cys Leu Asp Ile Arg Met Glu Gln Cys Tyr Leu Lys Trp Asp Glu
995 1000 1005

Asp Glu Cys Ile His Pro Val Pro Gly Lys Phe Arg Met Asp Ala Cys
1010 1015 1020

Cys Cys Ala Val Gly Ala Ala Trp Gly Thr Glu Cys Glu Glu Cys Pro
1025 1030 1035 1040

Lys Pro Gly Thr Lys Glu Tyr Glu Thr Leu Cys Pro Arg Gly Ala Gly
1045 1050 1055

Phe Ala Asn Arg Gly Asp Val Leu Thr Gly Arg Pro Phe Tyr Lys Asp
1060 1065 1070

Ile Asn Glu Cys Lys Ala Phe Pro Gly Met Cys Thr Tyr Gly Lys Cys
1075 1080 1085

Arg Asn Thr Ile Gly Ser Phe Lys Cys Arg Cys Asn Ser Gly Phe Ala
1090 1095 1100

Leu Asp Met Glu Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys Arg Ile
1105 1110 1115 1120

Ser Pro Asp Leu Cys Gly Ser Gly Ile Cys Val Asn Thr Pro Gly Ser
1125 1130 1135

Phe Glu Cys Glu Cys Phe Glu Gly Tyr Glu Ser Gly Phe Met Met Met
1140 1145 1150

Lys Asn Cys Met Asp Ile Asp Gly Cys Glu Arg Asn Pro Leu Leu Cys
1155 1160 1165

Arg Gly Gly Thr Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Asp Cys
1170 1175 1180

Pro Leu Gly His Glu Leu Ser Pro Ser Arg Glu Asp Cys Val Asp Ile
1185 1190 1195 1200

Asn Glu Cys Ser Leu Ser Asp Asn Leu Cys Arg Asn Gly Lys Cys Val
1205 1210 1215

Asn Met Ile Gly Thr Tyr Gln Cys Ser Cys Asn Pro Gly Tyr Gln Ala
1220 1225 1230

Thr Pro Asp Arg Gln Gly Cys Thr Asp Ile Asp Glu Cys Met Ile Met
1235 1240 1245

Asn Gly Gly Cys Asp Thr Gln Cys Thr Asn Ser Glu Gly Ser Tyr Glu
1250 1255 1260

Cys Ser Cys Ser Glu Gly Tyr Ala Leu Met Pro Asp Gly Arg Ser Cys
1265 1270 1275 1280

Ala Asp Ile Asp Glu Cys Glu Asn Asn Pro Asp Ile Cys Asp Gly Gly
1285 1290 1295

Gln Cys Thr Asn Ile Pro Gly Glu Tyr Arg Cys Leu Cys Tyr Asp Gly
1300 1305 1310

Phe Met Ala Ser Met Asp Met Lys Thr Cys Ile Asp Val Asn Glu Cys
1315 1320 1325

Asp Leu Asn Ser Asn Ile Cys Met Phe Gly Glu Cys Glu Asn Thr Lys
1330 1335 1340

Gly Ser Phe Ile Cys His Cys Gln Leu Gly Tyr Ser Val Lys Lys Gly
1345 1350 1355 1360

Thr Thr Gly Cys Thr Asp Val Asp Glu Cys Glu Ile Gly Ala His Asn
 1365 1370 1375

 Cys Asp Met His Ala Ser Cys Leu Asn Ile Pro Gly Ser Phe Lys Cys
 1380 1385 1390

 Ser Cys Arg Glu Gly Trp Ile Gly Asn Gly Ile Lys Cys Ile Asp Leu
 1395 1400 1405

 Asp Glu Cys Ser Asn Gly Thr His Gln Cys Ser Ile Asn Ala Gln Cys
 1410 1415 1420

 Val Asn Thr Pro Gly Ser Tyr Arg Cys Ala Cys Ser Glu Gly Phe Thr
 1425 1430 1435 1440

 Gly Asp Gly Phe Thr Cys Ser Asp Val Asp Glu Cys Ala Glu Asn Ile
 1445 1450 1455

 Asn Leu Cys Glu Asn Gly Gln Cys Leu Asn Val Pro Gly Ala Tyr Arg
 1460 1465 1470

 Cys Glu Cys Glu Met Gly Phe Thr Pro Ala Ser Asp Ser Arg Ser Cys
 1475 1480 1485

 Gln Asp Ile Asp Glu Cys Ser Phe Gln Asn Ile Cys Val Ser Gly Thr
 1490 1495 1500

 Cys Asn Asn Leu Pro Gly Met Phe His Cys Ile Cys Asp Asp Gly Tyr
 1505 1510 1515 1520

 Glu Leu Asp Arg Thr Gly Gly Asn Cys Thr Asp Ile Asp Glu Cys Ala
 1525 1530 1535

 Asp Pro Ile Asn Cys Val Asn Gly Leu Cys Val Asn Thr Pro Gly Arg
 1540 1545 1550

 Tyr Glu Cys Asn Cys Pro Pro Asp Phe Gln Leu Asn Pro Thr Gly Val
 1555 1560 1565

 Gly Cys Val Asp Asn Arg Val Gly Asn Cys Tyr Leu Lys Phe Gly Pro
 1570 1575 1580

 Arg Gly Asp Gly Ser Leu Ser Cys Asn Thr Glu Ile Gly Val Gly Val
 1585 1590 1595 1600

 Ser Arg Ser Ser Cys Cys Ser Leu Gly Lys Ala Trp Gly Asn Pro
 1605 1610 1615

Cys Glu Thr Cys Pro Pro Val Asn Ser Thr Glu Tyr Tyr Thr Leu Cys
1620 1625 1630

Pro Gly Gly Glu Gly Phe Arg Pro Asn Pro Ile Thr Ile Ile Leu Glu
1635 1640 1645

Asp Ile Asp Glu Cys Gln Glu Leu Pro Gly Leu Cys Gln Gly Gly Asn
1650 1655 1660

Cys Ile Asn Thr Phe Gly Ser Phe Gln Cys Glu Cys Pro Gln Gly Tyr
1665 1670 1675 1680

Tyr Leu Ser Glu Asp Thr Arg Ile Cys Glu Asp Ile Asp Glu Cys Phe
1685 1690 1695

Ala His Pro Gly Val Cys Gly Pro Gly Thr Cys Tyr Asn Thr Leu Gly
1700 1705 1710

Asn Tyr Thr Cys Ile Cys Pro Pro Glu Tyr Met Gln Val Asn Gly Gly
1715 1720 1725

His Asn Cys Met Asp Met Arg Lys Ser Phe Cys Tyr Arg Ser Tyr Asn
1730 1735 1740

Gly Thr Thr Cys Glu Asn Glu Leu Pro Phe Asn Val Thr Lys Arg Met
1745 1750 1755 1760

Cys Cys Cys Thr Tyr Asn Val Gly Lys Ala Gly Asn Lys Pro Cys Glu
1765 1770 1775

Pro Cys Pro Thr Pro Gly Thr Ala Asp Phe Lys Thr Ile Cys Gly Asn
1780 1785 1790

Ile Pro Gly Phe Thr Phe Asp Ile His Thr Gly Lys Ala Val Asp Ile
1795 1800 1805

Asp Glu Cys Lys Glu Ile Pro Gly Ile Cys Ala Asn Gly Val Cys Ile
1810 1815 1820

Asn Gln Ile Gly Ser Phe Arg Cys Glu Cys Pro Thr Gly Phe Ser Tyr
1825 1830 1835 1840

Asn Asp Leu Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Ser Asn Gly
1845 1850 1855

Asp Asn Leu Cys Gln Arg Asn Ala Asp Cys Ile Asn Ser Pro Gly Ser
1860 1865 1870

Tyr Arg Cys Glu Cys Ala Ala Gly Phe Lys Leu Ser Pro Asn Gly Ala
 1875 1880 1885

 Cys Val Asp Arg Asn Glu Cys Leu Glu Ile Pro Asn Val Cys Ser His
 1890 1895 1900

 Gly Leu Cys Val Asp Leu Gln Gly Ser Tyr Gln Cys Ile Cys His Asn
 1905 1910 1915 1920

 Gly Phe Lys Ala Ser Gln Asp Gln Thr Met Cys Met Asp Val Asp Glu
 1925 1930 1935

 Cys Glu Arg His Pro Cys Gly Asn Gly Thr Cys Lys Asn Thr Val Gly
 1940 1945 1950

 Ser Tyr Asn Cys Leu Cys Tyr Pro Gly Phe Glu Leu Thr His Asn Asn
 1955 1960 1965

 Asp Cys Leu Asp Ile Asp Glu Cys Ser Ser Phe Phe Gly Gln Val Cys
 1970 1975 1980

 Arg Asn Gly Arg Cys Phe Asn Glu Ile Gly Ser Phe Lys Cys Leu Cys
 1985 1990 1995 2000

 Asn Glu Gly Tyr Glu Leu Thr Pro Asp Gly Lys Asn Cys Ile Asp Thr
 2005 2010 2015

 Asn Glu Cys Val Ala Leu Pro Gly Ser Cys Ser Pro Gly Thr Cys Gln
 2020 2025 2030

 Asn Leu Glu Gly Ser Phe Arg Cys Ile Cys Pro Pro Gly Tyr Glu Val
 2035 2040 2045

 Lys Ser Glu Asn Cys Ile Asp Ile Asn Glu Cys Asp Glu Asp Pro Asn
 2050 2055 2060

 Ile Cys Leu Phe Gly Ser Cys Thr Asn Thr Pro Gly Gly Phe Gln Cys
 2065 2070 2075 2080

 Leu Cys Pro Pro Gly Phe Val Leu Ser Asp Asn Gly Arg Arg Cys Phe
 2085 2090 2095

 Asp Thr Arg Gln Ser Phe Cys Phe Thr Asn Phe Glu Asn Gly Lys Cys
 2100 2105 2110

 Ser Val Pro Lys Ala Phe Asn Thr Thr Lys Ala Lys Cys Cys Cys Ser
 2115 2120 2125

Lys Met Pro Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Lys
2130 2135 2140

Asp Asp Glu Val Ala Phe Gln Asp Leu Cys Pro Tyr Gly His Gly Thr
2145 2150 2155 2160

Val Pro Ser Leu His Asp Thr Arg Glu Asp Val Asn Glu Cys Leu Glu
2165 2170 2175

Ser Pro Gly Ile Cys Ser Asn Gly Gln Cys Ile Asn Thr Asp Gly Ser
2180 2185 2190

Phe Arg Cys Glu Cys Pro Met Gly Tyr Asn Leu Asp Tyr Thr Gly Val
2195 2200 2205

Arg Cys Val Asp Thr Asp Glu Cys Ser Ile Gly Asn Pro Cys Gly Asn
2210 2215 2220

Gly Thr Cys Thr Asn Val Ile Gly Ser Phe Glu Cys Asn Cys Asn Glu
2225 2230 2235 2240

Gly Phe Glu Pro Gly Pro Met Met Asn Cys Glu Asp Ile Asn Glu Cys
2245 2250 2255

Ala Gln Asn Pro Leu Leu Cys Ala Leu Arg Cys Met Asn Thr Phe Gly
2260 2265 2270

Ser Tyr Glu Cys Thr Cys Pro Ile Gly Tyr Ala Leu Arg Glu Asp Gln
2275 2280 2285

Lys Met Cys Lys Asp Leu Asp Glu Cys Ala Glu Gly Leu His Asp Cys
2290 2295 2300

Glu Ser Arg Gly Met Met Cys Lys Asn Leu Ile Gly Thr Phe Met Cys
2305 2310 2315 2320

Ile Cys Pro Pro Gly Met Ala Arg Arg Pro Asp Gly Glu Gly Cys Val
2325 2330 2335

Asp Glu Asn Glu Cys Arg Thr Lys Pro Gly Ile Cys Glu Asn Gly Arg
2340 2345 2350

Cys Val Asn Ile Ile Gly Ser Tyr Arg Cys Glu Cys Asn Glu Gly Phe
2355 2360 2365

Gln Ser Ser Ser Ser Gly Thr Glu Cys Leu Asp Asn Arg Gln Gly Leu
2370 2375 2380

Cys Phe Ala Glu Val Leu Gln Thr Ile Cys Gln Met Ala Ser Ser Ser
2385 2390 2395 2400

Arg Asn Leu Val Thr Lys Ser Glu Cys Cys Cys Asp Gly Gly Arg Gly
2405 2410 2415

Trp Gly His Gln Cys Glu Leu Cys Pro Leu Pro Gly Thr Ala Gln Tyr
2420 2425 2430

Lys Lys Ile Cys Pro His Gly Pro Gly Tyr Thr Thr Asp Gly Arg Asp
2435 2440 2445

Ile Asp Glu Cys Lys Val Met Pro Asn Leu Cys Thr Asn Gly Gln Cys
2450 2455 2460

Ile Asn Thr Met Gly Ser Phe Arg Cys Phe Cys Lys Val Gly Tyr Thr
2465 2470 2475 2480

Thr Asp Ile Ser Gly Thr Ser Cys Ile Asp Leu Asp Glu Cys Ser Gln
2485 2490 2495

Ser Pro Lys Pro Cys Asn Tyr Ile Cys Lys Asn Thr Glu Gly Ser Tyr
2500 2505 2510

Gln Cys Ser Cys Pro Arg Gly Tyr Val Leu Gln Glu Asp Gly Lys Thr
2515 2520 2525

Cys Lys Asp Leu Asp Glu Cys Gln Thr Lys Gln His Asn Cys Gln Phe
2530 2535 2540

Leu Cys Val Asn Thr Leu Gly Gly Phe Thr Cys Lys Cys Pro Pro Gly
2545 2550 2555 2560

Phe Thr Gln His His Thr Ala Cys Ile Asp Asn Asn Glu Cys Gly Ser
2565 2570 2575

Gln Pro Leu Leu Cys Gly Lys Gly Ile Cys Gln Asn Thr Pro Gly
2580 2585 2590

Ser Phe Ser Cys Glu Cys Gln Arg Gly Phe Ser Leu Asp Ala Thr Gly
2595 2600 2605

Leu Asn Cys Glu Asp Val Asp Glu Cys Asp Gly Asn His Arg Cys Gln
2610 2615 2620

His Gly Cys Gln Asn Ile Leu Gly Gly Tyr Arg Cys Gly Cys Pro Gln
2625 2630 2635 2640

Gly Tyr Ile Gln His Tyr Gln Trp Asn Gln Cys Val Asp Glu Asn Glu
2645 2650 2655

Cys Ser Asn Pro Asn Ala Cys Gly Ser Ala Ser Cys Tyr Asn Thr Leu
2660 2665 2670

Gly Ser Tyr Lys Cys Ala Cys Pro Ser Gly Phe Ser Phe Asp Gln Phe
2675 2680 2685

Ser Ser Ala Cys His Asp Val Asn Glu Cys Ser Ser Ser Lys Asn Pro
2690 2695 2700

Cys Asn Tyr Gly Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly Cys
2705 2710 2715 2720

Pro Pro Gly Tyr Tyr Arg Val Gly Gln Gly His Cys Val Ser Gly Met
2725 2730 2735

Gly Phe Asn Lys Gly Gln Tyr Leu Ser Leu Asp Thr Glu Val Asp Glu
2740 2745 2750

Glu Asn Ala Leu Ser Pro Glu Ala Cys Tyr Glu Cys Lys Ile Asn Gly
2755 2760 2765

Tyr Pro Lys Lys Asp Ser Arg Gln Lys Arg Ser Ile His Glu Pro Asp
2770 2775 2780

Pro Thr Ala Val Glu Gln Ile Ser Leu Glu Ser Val Asp Met Asp Ser
2785 2790 2795 2800

Pro Val Asn Met Lys Phe Asn Leu Ser His Leu Gly Ser Lys Glu His
2805 2810 2815

Ile Leu Glu Leu Arg Pro Ala Ile Gln Pro Leu Asn Asn His Ile Arg
2820 2825 2830

Tyr Val Ile Ser Gln Gly Asn Asp Asp Ser Val Phe Arg Ile His Gln
2835 2840 2845

Arg Asn Gly Leu Ser Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro
2850 2855 2860

Gly Thr Tyr Thr Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys
2865 2870 2875 2880

Glu Leu Lys Lys Leu Glu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly
2885 2890 2895

Glu Leu Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr
2900 2905 2910

<210> 69
<211> 2135
<212> DNA
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<400> 69
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tccccttc cagtccactt cgactgctca ggaaagtaca gatgtcgctc atcccttaag 120
tgtatcgagc tgatacgctcg atgtgacgga gtctcgatt gcaaagacgg ggaggacgag 180
taccgctgtg tccgggtggg tggtcagaat gccgtgctcc aggtgttcac agctgcttcg 240
tggaaagacca tgtgctccga tgactggaag ggtcaactacg caaatgttgc ctgtgcccaa 300
ctgggttcc caagctatgt gagttcagat aacctcagag tgagctcgct ggagggcag 360
ttccgggagg agtttggtc catcgatcac ctcttgcag atgacaaggt gactgcatta 420
caccactca gatatgttag ggagggatgt gcctctggcc acgtggttac cttgcagtgc 480
acagcctgtg gtcatagaag gggctacagc tcacgcacg tgggtggaaa catgccttg 540
ctctcgca ggcctggca ggccagcctt cagttccagg gctaccacct gtgcggggc 600
tctgtcatca cggccctgtg gatcatca gctgcacact gtgttatga cttgtacctc 660
cccaagtcat ggaccatcca ggtgggtcta gttccctgt tggacaatcc agccccatcc 720
cacttggtg agaagattgt ctaccacagc aagtacaagc caaaagaggt gggcaatgac 780
atcgccctta tgaagctggc cgggccactc acgttcaatg aaatgatcca gcctgtgtgc 840
ctgccaact ctgaagagaa cttcccccgt gaaaaagtgt gctggacgtc aggatgggg 900
gccacagagg atggagcagg tgacgcctcc cctgtcctga accacgcggc cgtcccttg 960
atttccaaca agatctgcaa ccacagggac gtgtacggc gcatcatctc cccctccatg 1020
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ctgggtgtc aagagaggag gctgtggaa ttagtggag cgaccagctt tggcatcgcc 1140
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cacgagcaga tggagagaga cctaaaaacc tgaagaggaa gggacaagt agccacctga 1260
gttcctgagg tgatgaagac agcccgatcc tcccctggac tcccgtgtag gaacctgcac 1320
acgagcagac acccttggag ctctgagttc cggcaccagt agcaggcccg aaagaggcac 1380
ccttccatct gattccagca caaccttcaa gctgtttt gtttttgtt ttttgaggt 1440
ggagtctcgc tctgtgccc aggctggagt gcagtggcga aatccctgt cactgcagcc 1500
tccgcttccc tggtaaagc gattctctt cctcagcttc cccagtagct gggaccacag 1560
gtgcccggca ccacacccaa ctaattttt tatttttagt agagacaggg tttcaccatg 1620
ttggccaggc tgctctaaa cccctgaccc caaatgatgt gcctgttca gcctccaca 1680
gtgctggat tacaggcatg ggccaccacg cctagcctca cgctccttc tgatctcac 1740
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ctctccaggc gtcttgc当地 acccgatggcc agataaggcag ttatgtgacc tcacgtgca 1860
agccaccaac agccactcag aaaagacgca ccagcccaga agtgcagaac tgcagtcact 1920
gcacgtttc atctctaggc accagaacca aaccacccct ttctacttcc aagacttatt 1980
ttcacatgtg gggaggtta tcttaggaatg actcgtaaa ggcctattt catgatttct 2040
ttgttagcatt tgggtgttga cgtattattt tccttgatt ccaaataata tgttccttc 2100
cctcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 2135

<210> 70
<211> 790
<212> PRT
<213> Sus scrofa

<400> 70
Asp Ser Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Phe Leu Phe Ser
1 5 10 15

Leu Ser Arg Lys Gln Val Ala Ala Arg Ser Val Glu Glu Cys Ala Ala
20 25 30

Lys Cys Glu Ala Glu Thr Asn Phe Ile Cys Arg Ala Phe Gln Tyr His
35 40 45

Ser Lys Asp Gln Gln Cys Val Val Met Ala Glu Asn Ser Lys Thr Ser
50 55 60

Pro Ile Ala Arg Met Arg Asp Val Val Leu Phe Glu Lys Arg Ile Tyr
65 70 75 80

Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Thr
85 90 95

Ser Lys Thr Lys Ser Gly Val Ile Cys Gln Lys Trp Ser Val Ser Ser
100 105 110

Pro His Ile Pro Lys Tyr Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu
115 120 125

Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Lys Gly Pro Trp
130 135 140

Cys Tyr Thr Thr Asp Pro Glu Thr Arg Phe Asp Tyr Cys Asp Ile Pro
145 150 155 160

Glu Cys Glu Asp Glu Cys Met His Cys Ser Gly Glu His Tyr Glu Gly
165 170 175

Lys Ile Ser Lys Thr Met Ser Gly Ile Glu Cys Gln Ser Trp Gly Ser
180 185 190

Gln Ser Pro His Ala His Gly Tyr Leu Pro Ser Lys Phe Pro Asn Lys
195 200 205

Asn Leu Lys Met Asn Tyr Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro
210 215 220

Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	Lys	Arg	Trp	Glu	Phe	Cys	Asp	Ile
225			230					235						240	
Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Thr	Ser	Gly	Pro	Thr	Tyr	Gln	Cys
	245				250								255		
Leu	Lys	Gly	Arg	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Val	Ser	Val	Thr	Ala
	260				265								270		
Ser	Gly	His	Thr	Cys	Gln	Arg	Trp	Ser	Ala	Gln	Ser	Pro	His	Lys	His
	275				280								285		
Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Glu	Glu	Asn	Tyr
	290				295								300		
Cys	Arg	Asn	Pro	Asp	Gly	Glu	Thr	Ala	Pro	Trp	Cys	Tyr	Thr	Thr	Asp
	305				310								315		320
Ser	Glu	Val	Arg	Trp	Asp	Tyr	Cys	Lys	Ile	Pro	Ser	Cys	Gly	Ser	Ser
		325							330				335		
Thr	Thr	Ser	Thr	Glu	His	Leu	Asp	Ala	Pro	Val	Pro	Pro	Glu	Gln	Thr
			340					345					350		
Pro	Val	Ala	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Glu	Ser	Tyr	Arg	Gly
			355					360					365		
Thr	Ser	Ser	Thr	Thr	Ile	Thr	Gly	Arg	Lys	Cys	Gln	Ser	Trp	Val	Ser
			370					375					380		
Met	Thr	Pro	His	Arg	His	Glu	Lys	Thr	Pro	Gly	Asn	Phe	Pro	Asn	Ala
			385					390					395		400
Gly	Leu	Thr	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Asp	Lys	Ser	Pro
					405				410				415		
Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Arg	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu
					420				425				430		
Lys	Lys	Cys	Ser	Glu	Thr	Glu	Gln	Gln	Val	Thr	Asn	Phe	Pro	Ala	Ile
					435				440				445		
Ala	Gln	Val	Pro	Ser	Val	Glu	Asp	Leu	Ser	Glu	Asp	Cys	Met	Phe	Gly
								450					460		
Asn	Gly	Lys	Arg	Tyr	Arg	Gly	Lys	Arg	Ala	Thr	Thr	Val	Ala	Gly	Val
					465				470				475		480

Pro Cys Gln Glu Trp Ala Ala Gln Glu Pro His Arg His Ser Ile Phe
485 490 495

Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys Asn Tyr Cys Arg
500 505 510

Asn Pro Asp Gly Asp Asp Asn Gly Pro Trp Cys Tyr Thr Thr Asn Pro
515 520 525

Gln Lys Leu Phe Asp Tyr Cys Asp Val Pro Gln Cys Val Thr Ser Ser
530 535 540

Phe Asp Cys Gly Lys Pro Lys Val Glu Pro Lys Lys Cys Pro Ala Arg
545 550 555 560

Val Val Gly Gly Cys Val Ser Ile Pro His Ser Trp Pro Trp Gln Ile
565 570 575

Ser Leu Arg Tyr Arg Tyr Arg Gly His Phe Cys Gly Gly Thr Leu Ile
580 585 590

Ser Pro Glu Trp Val Leu Thr Ala Lys His Cys Leu Glu Lys Ser Ser
595 600 605

Ser Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Glu Glu Tyr His
610 615 620

Leu Gly Glu Gly Val Gln Glu Ile Asp Val Ser Lys Leu Phe Lys Glu
625 630 635 640

Pro Ser Glu Ala Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val
645 650 655

Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Thr Pro Asn Tyr Val
660 665 670

Val Ala Asp Arg Thr Ala Cys Tyr Ile Thr Gly Trp Gly Glu Thr Lys
675 680 685

Gly Thr Tyr Gly Ala Gly Leu Leu Lys Glu Ala Arg Leu Pro Val Ile
690 695 700

Glu Asn Lys Val Cys Asn Arg Tyr Glu Tyr Leu Gly Gly Lys Val Ser
705 710 715 720

Pro Asn Glu Leu Cys Ala Gly His Leu Ala Gly Gly Ile Asp Ser Cys
725 730 735

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr
740 745 750

Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Leu Pro Asn
755 760 765

Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu
770 775 780

Glu Ile Met Arg Arg Asn
785 790

<210> 71
<211> 812
<212> PRT
<213> Bos taurus

<400> 71
Met Leu Pro Ala Ser Pro Lys Met Glu His Lys Ala Val Val Phe Leu
1 5 10 15

Leu Leu Leu Phe Leu Lys Ser Gly Leu Gly Asp Leu Leu Asp Asp Tyr
20 25 30

Val Asn Thr Gln Gly Ala Ser Leu Leu Ser Leu Ser Arg Lys Asn Leu
35 40 45

Ala Gly Arg Ser Val Glu Asp Cys Ala Ala Lys Cys Glu Glu Glu Thr
50 55 60

Asp Phe Val Cys Arg Ala Phe Gln Tyr His Ser Lys Glu Gln Gln Cys
65 70 75 80

Val Val Met Ala Glu Asn Ser Lys Asn Thr Pro Val Phe Arg Met Arg
85 90 95

Asp Val Ile Leu Tyr Glu Lys Arg Ile Tyr Leu Leu Glu Cys Lys Thr
100 105 110

Gly Asn Gly Gln Thr Tyr Arg Gly Thr Thr Ala Glu Thr Lys Ser Gly
115 120 125

Val Thr Cys Gln Lys Trp Ser Ala Thr Ser Pro His Val Pro Lys Phe
130 135 140

Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu Glu Glu Asn Tyr Cys Arg

145 150 155 160
Asn Pro Asp Asn Asp Glu Asn Gly Pro Trp Cys Tyr Thr Thr Asp Pro
165 170 175

Asp Lys Arg Tyr Asp Tyr Cys Asp Ile Pro Glu Cys Glu Asp Lys Cys
180 185 190

Met His Cys Ser Gly Glu Asn Tyr Glu Gly Lys Ile Ala Lys Thr Met
195 200 205

Ser Gly Arg Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His
210 215 220

Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Met Asn Tyr
225 230 235 240

Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp
245 250 255

Pro Gln Lys Arg Trp Glu Phe Cys Asp Ile Pro Arg Cys Thr Thr Pro
260 265 270

Pro Pro Ser Ser Gly Pro Lys Tyr Gln Cys Leu Lys Gly Thr Gly Lys
275 280 285

Asn Tyr Gly Gly Thr Val Ala Val Thr Glu Ser Gly His Thr Cys Gln
290 295 300

Arg Trp Ser Glu Gln Thr Pro His Lys His Asn Arg Thr Pro Glu Asn
305 310 315 320

Phe Pro Cys Lys Asn Leu Glu Asn Tyr Cys Arg Asn Pro Asn Gly
325 330 335

Glu Lys Ala Pro Trp Cys Tyr Thr Thr Asn Ser Glu Val Arg Trp Glu
340 345 350

Tyr Cys Thr Ile Pro Ser Cys Glu Ser Ser Pro Leu Ser Thr Glu Arg
355 360 365

Met Asp Val Pro Val Pro Pro Glu Gln Thr Pro Val Pro Gln Asp Cys
370 375 380

Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr Ile
385 390 395 400

Thr Gly Arg Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg His

405	410	415
Leu Lys Thr Pro Glu Asn Tyr Pro Asn Ala Gly Leu Thr Met Asn Tyr		
420	425	430
Cys Arg Asn Pro Asp Ala Asp Lys Ser Pro Trp Cys Tyr Thr Thr Asp		
435	440	445
Pro Arg Val Arg Trp Glu Phe Cys Asn Leu Lys Lys Cys Ser Glu Thr		
450	455	460
Pro Glu Gln Val Pro Ala Ala Pro Gln Ala Pro Gly Val Glu Asn Pro		
465	470	475
480		
Pro Glu Ala Asp Cys Met Ile Gly Thr Gly Lys Ser Tyr Arg Gly Lys		
485	490	495
Lys Ala Thr Thr Val Ala Gly Val Pro Cys Gln Glu Trp Ala Ala Gln		
500	505	510
Glu Pro His Gln His Ser Ile Phe Thr Pro Glu Thr Asn Pro Gln Ser		
515	520	525
Gly Leu Glu Arg Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Asn Gly		
530	535	540
Pro Trp Cys Tyr Thr Met Asn Pro Arg Lys Pro Phe Asp Tyr Cys Asp		
545	550	555
560		
Val Pro Gln Cys Glu Ser Ser Phe Asp Cys Gly Lys Pro Lys Val Glu		
565	570	575
Pro Lys Lys Cys Ser Gly Arg Ile Val Gly Gly Cys Val Ser Lys Pro		
580	585	590
His Ser Trp Pro Trp Gln Val Ser Leu Arg Arg Ser Ser Arg His Phe		
595	600	605
Cys Gly Gly Thr Leu Ile Ser Pro Lys Trp Val Leu Thr Ala Ala His		
610	615	620
Cys Leu Asp Asn Ile Leu Ala Leu Ser Phe Tyr Lys Val Ile Leu Gly		
625	630	635
640		
Ala His Asn Glu Lys Val Arg Glu Gln Ser Val Gln Glu Ile Pro Val		
645	650	655
Ser Arg Leu Phe Arg Glu Pro Ser Gln Ala Asp Ile Ala Leu Leu Lys		

660 665 670
Leu Ser Arg Pro Ala Ile Ile Thr Lys Glu Val Ile Pro Ala Cys Leu
675 680 685

Pro Pro Pro Asn Tyr Met Val Ala Ala Arg Thr Glu Cys Tyr Ile Thr
690 695 700

Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Glu Gly Leu Leu Lys Glu
705 710 715 720

Ala His Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Asn Glu Tyr
725 730 735

Leu Asp Gly Arg Val Lys Pro Thr Glu Leu Cys Ala Gly His Leu Ile
740 745 750

Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
755 760 765

Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
770 775 780

Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Pro
785 790 795 800

Tyr Val Pro Trp Ile Glu Glu Thr Met Arg Arg Asn
805 810

<210> 72
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus
Sequence

<400> 72
Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser
20 25 30

Leu Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly
35 40 45

Ser Asp Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 50 55 60

 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65 70 75 80

 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
 85 90 95

 Lys Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
 100 105 110

 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125

 Trp Gly Arg Thr Ser Glu Ser Gly Gly Ser Leu Pro Asp Thr Leu Gln
 130 135 140

 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
 145 150 155 160

 Ser Gly Gly Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu Glu
 165 170 175

 Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 180 185 190

 Asn Asp Asn Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser Asp
 195 200 205

 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser
 210 215 220

 Tyr Leu Asp Trp Ile
 225

<210> 73
 <211> 2646
 <212> DNA
 <213> Homo sapiens

<400> 73
 atcagcaaca attaaaatat tcacgtggta tctgttagttt aataatggac caacatcaac 60
 atttgaataa aacagcagag tcagcatctt cagagaaaaaa gaaaacaaga cgctgcaatg 120
 gattcaagat gttcttggca gccctgtcat tcagctatat tgctaaagca ctaggtggaa 180
 tcattatgaa aatttccatc actcaaatacg aaaggagatt tgacatatcc tcttcttgc 240

<210> 74
<211> 691
<212> PRT
<213> Homo sapiens

<400> 74

Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu Ala Gln Pro Ser
1 5 10 15

Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
20 25 30

Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
35 40 45

Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
50 55 60

Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
65 70 75 80

Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
85 90 95

Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
100 105 110

Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
115 120 125

Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
130 135 140

Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
145 150 155 160

Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
165 170 175

Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
180 185 190

Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
195 200 205

Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
210 215 220

Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
225 230 235 240

Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
245 250 255

Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
260 265 270

Ser Ile Pro Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
275 280 285

Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
290 295 300

Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
305 310 315 320

Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
325 330 335

Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
340 345 350

Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
355 360 365

Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
370 375 380

Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
385 390 395 400

Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
405 410 415

Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
420 425 430

Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
435 440 445

Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
450 455 460

Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
465 470 475 480

Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
485 490 495

Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
500 505 510

Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
 515 520 525

 Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
 530 535 540

 Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val
 545 550 555 560

 Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser
 565 570 575

 Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly
 580 585 590

 Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly
 595 600 605

 Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val
 610 615 620

 Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr
 625 630 635 640

 Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile
 645 650 655

 Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser
 660 665 670

 Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu
 675 680 685

 Thr His Cys
 690

<210> 75
 <211> 204
 <212> DNA
 <213> Rattus norvegicus

<400> 75
 ggctgaggag gaggccgcgg cagcggagtt gcgtggagaa cacacgctca ctgagaagtt 60
 tgtctgcttg gatcactcct tcgggcatga ctgcagccta acctgcgatg actgcaggaa 120
 tggggggact tgctccccgg gccaggacgg ctgtgactgc ccagaggct ggactggaat 180
 catctgcaat gagacttgc ctcc 204

<210> 76
<211> 91
<212> DNA
<213> Rattus norvegicus

<400> 76
tggatggacccatggatggccgg ctgcgcctttg tgcgccccct gccccacatt gcgggtgctga 60
ggatgagct gcccccactc ttccaggatg a 91

<210> 77
<211> 1574
<212> PRT
<213> Rattus norvegicus

<400> 77
Met Pro Val Arg Ala Glu Ala Arg Ala Ala Trp Arg Val Val Ala Leu
1 5 10 15

Ala Leu Leu Leu Leu Pro Ala Met Pro Ala Ala Ser Pro Pro Leu Thr
20 25 30

Pro Arg Pro Leu Gln Pro Ser Met Pro His Val Cys Ala Glu Gln Lys
35 40 45

Leu Thr Leu Val Gly His Arg Gln Pro Cys Val Gln Ala Phe Ser Arg
50 55 60

Ile Val Pro Val Trp Arg Arg Thr Gly Cys Ala Gln Gln Ala Trp Cys
65 70 75 80

Ile Gly Gln Glu Arg Arg Thr Val Tyr Tyr Met Ser Tyr Arg Gln Val
85 90 95

Tyr Ala Thr Glu Ala Arg Thr Val Phe Arg Cys Cys Pro Gly Trp Ser
100 105 110

Gln Lys Pro Gly Gln Glu Gly Cys Leu Ser Asp Val Asp Glu Cys Ala
115 120 125

Ser Ala Asn Gly Gly Cys Glu Gly Pro Cys Cys Asn Thr Val Gly Gly
130 135 140

Phe Tyr Cys Arg Cys Pro Pro Gly Tyr Gln Leu Gln Gly Asp Gly Lys
145 150 155 160

Thr Cys Gln Asp Val Asp Glu Cys Arg Ala His Asn Gly Gly Cys Gln
165 170 175

His Arg Cys Val Asn Thr Pro Gly Ser Tyr Leu Cys Glu Cys Lys Pro
180 185 190

Gly Phe Arg Leu His Thr Asp Gly Arg Thr Cys Leu Ala Ile Ser Ser
195 200 205

Cys Thr Leu Gly Asn Gly Gly Cys Gln His Gln Cys Val Gln Leu Thr
210 215 220

Val Thr Gln His Arg Cys Gln Cys Arg Pro Gln Tyr Gln Leu Gln Glu
225 230 235 240

Asp Gly Arg Arg Cys Val Arg Arg Ser Pro Cys Ala Glu Gly Asn Gly
245 250 255

Gly Cys Met His Ile Cys Gln Glu Leu Arg Gly Leu Ala His Cys Gly
260 265 270

Cys His Pro Gly Tyr Gln Leu Ala Ala Asp Arg Lys Thr Cys Glu Asp
275 280 285

Val Asp Glu Cys Ala Leu Gly Leu Ala Gln Cys Ala His Gly Cys Leu
290 295 300

Asn Thr Gln Gly Ser Phe Lys Cys Val Cys His Ala Gly Tyr Glu Leu
305 310 315 320

Gly Ala Asp Gly Arg Gln Cys Tyr Arg Ile Glu Met Glu Ile Val Asn
325 330 335

Ser Cys Glu Ala Gly Asn Gly Gly Cys Ser His Gly Cys Ser His Thr
340 345 350

Ser Thr Gly Pro Leu Cys Thr Cys Pro Arg Gly Tyr Glu Leu Asp Glu
355 360 365

Asp Gln Lys Thr Cys Ile Asp Ile Asp Asp Cys Ala Asn Ser Pro Cys
370 375 380

Cys Gln Gln Ala Cys Ala Asn Thr Pro Gly Gly Tyr Glu Cys Ser Cys
385 390 395 400

Phe Ala Gly Tyr Arg Leu Asn Thr Asp Gly Cys Gly Cys Glu Asp Val
405 410 415

Asp Glu Cys Ala Ser Gly His Gly Gly Cys Glu His His Cys Ser Asn
420 425 430

Leu Ala Gly Ser Phe Gln Cys Phe Cys Glu Ala Gly Tyr Arg Leu Asp
435 440 445

Glu Asp Arg Arg Gly Cys Thr Ser Leu Glu Glu Ser Val Val Asp Leu
450 455 460

Asp Gly Arg Leu Pro Phe Val Arg Pro Leu Pro His Ile Ala Val Leu
465 470 475 480

Arg Asp Glu Leu Pro Arg Leu Phe Gln Asp Asp Tyr Gly Ala Glu Glu
485 490 495

Glu Ala Ala Ala Ala Glu Leu Arg Gly Glu His Thr Leu Thr Glu Lys
500 505 510

Phe Val Cys Leu Asp His Ser Phe Gly His Asp Cys Ser Leu Thr Cys
515 520 525

Asp Asp Cys Arg Asn Gly Gly Thr Cys Phe Pro Gly Gln Asp Gly Cys
530 535 540

Asp Cys Pro Glu Gly Trp Thr Gly Ile Ile Cys Asn Glu Thr Cys Pro
545 550 555 560

Pro Asp Thr Phe Gly Lys Asn Cys Ser Ser Pro Cys Thr Cys Gln Asn
565 570 575

Gly Gly Thr Cys Asp Pro Val Leu Gly Ala Cys Arg Cys Pro Pro Gly
580 585 590

Val Ser Gly Ala His Cys Glu Asp Gly Cys Pro Lys Gly Phe Tyr Gly
595 600 605

Lys His Cys Arg Lys Cys His Cys Ala Asn Arg Gly Arg Cys His
610 615 620

Arg Leu Tyr Gly Ala Cys Leu Cys Asp Pro Gly Leu Tyr Gly Arg Phe
625 630 635 640

Cys His Leu Ala Cys Pro Pro Trp Ala Phe Gly Pro Gly Cys Ser Glu
645 650 655

Asp Cys Leu Cys Glu Gln Ser His Thr Arg Ser Cys Asn Pro Lys Asp
660 665 670

Gly Ser Cys Ser Cys Lys Ala Gly Phe Gln Gly Glu Arg Cys Gln Ala
675 680 685

Glu Cys Glu Ser Gly Phe Phe Gly Pro Gly Cys Arg His Arg Cys Thr
690 695 700

Cys Gln Pro Gly Val Ala Cys Asp Pro Val Ser Gly Glu Cys Arg Thr
705 710 715 720

Gln Cys Pro Pro Gly Tyr Gln Gly Glu Asp Cys Gly Gln Glu Cys Pro
725 730 735

Val Gly Thr Phe Gly Val Asn Cys Ser Gly Ser Cys Ser Cys Val Gly
740 745 750

Ala Pro Cys His Arg Val Thr Gly Glu Cys Leu Cys Pro Pro Gly Lys
755 760 765

Thr Gly Glu Asp Cys Gly Ala Asp Cys Pro Glu Gly Arg Trp Gly Leu
770 775 780

Gly Cys Gln Glu Ile Cys Pro Ala Cys Glu His Gly Ala Ser Cys Asn
785 790 795 800

Pro Glu Thr Gly Thr Cys Leu Cys Leu Pro Gly Phe Val Gly Ser Arg
805 810 815

Cys Gln Asp Thr Cys Ser Ala Gly Trp Tyr Gly Thr Gly Cys Gln Ile
820 825 830

Arg Cys Ala Cys Ala Asn Asp Gly His Cys Asp Pro Thr Thr Gly Arg
835 840 845

Cys Ser Cys Ala Pro Gly Trp Thr Gly Leu Ser Cys Gln Arg Ala Cys
850 855 860

Asp Ser Gly His Trp Gly Pro Asp Cys Ile His Pro Cys Asn Cys Ser
865 870 875 880

Ala Gly His Gly Asn Cys Asp Ala Val Ser Gly Leu Cys Leu Cys Glu
885 890 895

Ala Gly Tyr Glu Gly Pro Arg Cys Glu Gln Ser Cys Arg Gln Gly Tyr
900 905 910

Tyr Gly Pro Ser Cys Glu Gln Lys Cys Arg Cys Glu His Gly Ala Ala
915 920 925

Cys Asp His Val Ser Gly Ala Cys Thr Cys Pro Ala Gly Trp Arg Gly
930 935 940

Ser Phe Cys Glu His Ala Cys Pro Ala Gly Phe Phe Gly Leu Asp Cys
945 950 955 960

Asp Ser Ala Cys Asn Cys Ser Ala Gly Ala Pro Cys Asp Ala Val Thr
965 970 975

Gly Ser Cys Ile Cys Pro Ala Gly Arg Trp Gly Pro Arg Cys Ala Gln
980 985 990

Ser Cys Pro Pro Leu Thr Phe Gly Leu Asn Cys Ser Gln Ile Cys Thr
995 1000 1005

Cys Phe Asn Gly Ala Ser Cys Asp Ser Val Thr Gly Gln Cys His Cys
1010 1015 1020

Ala Pro Gly Trp Met Gly Pro Thr Cys Leu Gln Ala Cys Pro Pro Gly
1025 1030 1035 1040

Leu Tyr Gly Lys Asn Cys Gln His Ser Cys Leu Cys Arg Asn Gly Gly
1045 1050 1055

Arg Cys Asp Pro Ile Leu Gly Gln Cys Thr Cys Pro Glu Gly Trp Thr
1060 1065 1070

Gly Leu Ala Cys Glu Asn Glu Cys Leu Pro Gly His Tyr Ala Ala Gly
1075 1080 1085

Cys Gln Leu Asn Cys Ser Cys Leu His Gly Gly Ile Cys Asp Arg Leu
1090 1095 1100

Thr Gly His Cys Leu Cys Pro Ala Gly Trp Thr Gly Asp Lys Cys Gln
1105 1110 1115 1120

Ser Ser Cys Val Ser Gly Thr Phe Gly Val His Cys Glu Glu His Cys
1125 1130 1135

Ala Cys Arg Lys Gly Ala Ser Cys His His Val Thr Gly Ala Cys Phe
1140 1145 1150

Cys Pro Pro Gly Trp Arg Gly Pro His Cys Glu Gln Ala Cys Pro Arg
1155 1160 1165

Gly Trp Phe Gly Glu Ala Cys Ala Gln Arg Cys Leu Cys Pro Thr Asn
1170 1175 1180

Ala Ser Cys His His Val Thr Gly Glu Cys Arg Cys Pro Pro Gly Phe
1185 1190 1195 1200

Thr Gly Leu Ser Cys Glu Gln Ala Cys Gln Pro Gly Thr Phe Gly Lys
1205 1210 1215

Asp Cys Glu His Leu Cys Gln Cys Pro Gly Glu Thr Trp Ala Cys Asp
1220 1225 1230

Pro Ala Ser Gly Val Cys Thr Cys Ala Ala Gly Tyr His Gly Thr Gly
1235 1240 1245

Cys Leu Gln Arg Cys Pro Ser Gly Arg Tyr Gly Pro Gly Cys Glu His
1250 1255 1260

Ile Cys Lys Cys Leu Asn Gly Gly Thr Cys Asp Pro Ala Thr Gly Ala
1265 1270 1275 1280

Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp Cys Ser Leu Ala Cys
1285 1290 1295

Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His Val Cys Ala Cys Arg
1300 1305 1310

Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Ala Cys Ile Cys Ser Pro
1315 1320 1325

Gly Lys Thr Gly Val Arg Cys Glu His Gly Cys Pro Gln Asp Arg Phe
1330 1335 1340

Gly Lys Gly Cys Glu Leu Lys Cys Ala Cys Arg Asn Gly Gly Leu Cys
1345 1350 1355 1360

His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met Gly Pro
1365 1370 1375

His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala Cys Leu
1380 1385 1390

Leu Glu Cys Phe Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr Thr Gly
1395 1400 1405

Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu His Ser
1410 1415 1420

Cys Pro Ser Gly Phe His Gly Pro Gly Cys Gln Arg Val Cys Glu Cys
1425 1430 1435 1440

Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Gln Cys Leu Cys Pro
1445 1450 1455

Ala Gly Phe His Gly Gln Phe Cys Glu Lys Gly Cys Glu Ser Gly Ser
1460 1465 1470

Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys His Thr Gly Val Pro
1475 1480 1485

Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg Thr Gly
1490 1495 1500

Ala Ala Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro Gly Cys
1505 1510 1515 1520

Ala Leu Arg Cys Asp Cys Gly Gly Ala Asp Cys Asp Pro Ile Ser
1525 1530 1535

Gly Gln Cys His Cys Val Asp Ser Tyr Met Gly Pro Thr Cys Arg Glu
1540 1545 1550

Val Pro Thr Gln Ile Ser Ser Ser Arg Pro Ala Pro Gln His Pro Ser
1555 1560 1565

Ser Arg Ala Met Lys His
1570

<210> 78

<211> 1708

<212> DNA

<213> Homo sapiens

<400> 78

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<210> 79
 <211> 1151
 <212> PRT
 <213> Gallus gallus

<400> 79
 Arg Ser Pro Thr Pro Pro Pro Arg Asn Pro Pro Pro Thr Pro Pro Ala
 1 5 10 15

Pro Ser Pro Ala Pro Ala Pro Ala Pro Ala Pro Thr Ala Pro Pro Arg
 20 25 30

Pro Lys Trp Val Pro Ile Ala Glu Leu His Pro Ala Ala Pro Gln Pro
 35 40 45

Pro Pro Lys Trp Val Pro Ile Gly Gly Ala Pro Pro Pro Pro Gly Thr
 50 55 60

Glu Pro Thr Pro Pro Ser Lys Pro Thr Asp Gly Ala Asp Ala Ala Pro
 65 70 75 80

Lys Ala Ser Ala Glu Leu Thr Ser Pro Pro Pro Ala Ser Pro Ser Pro
 85 90 95

Pro Asp Gly Pro Lys Ala Pro Ser Gly Ala Gly Glu Ala Glu Ala Gly
 100 105 110

Thr Pro Pro Pro Ser Gln Gly Pro Ala Gly Thr Pro Pro Pro Ser Gln
 115 120 125

Gly Ala Ala Gly Ala Pro Lys Gly Asp Gly Thr Ala Gln Pro Ser Gly

130	135	140
Thr Lys Ser Gly Ala Asp Gly Lys Pro Ala Ala Gln Asp Val Pro Lys		
145	150	155
Ala Thr Thr Ala Ala Thr Glu Ala Arg Pro Ala Ser Ala Ala Ser Pro		
165	170	175
Thr Val Pro Lys Ala Thr Ala Glu Ala Thr Ala Val Thr Ala Ala Ser		
180	185	190
Gln Ser Ala Pro Lys Ala Ala Thr Asp Ala Ala Ala Val Thr Ala Ala		
195	200	205
Ser Gln Ser Ala Pro Lys Ala Thr Val Glu Val Lys Pro Ala Ala Ala		
210	215	220
Ala Val Ala Lys Glu Ala Lys Ala Val Thr Ala Ala Ala Ala Pro		
225	230	235
Lys Ala Thr Ala Glu Ala Lys Pro Ala Pro Val Thr Ser Pro Thr Ile		
245	250	255
Pro Cys Ser Ser Ala Glu Ala Lys Pro Leu Thr Ala Ala Ser Pro Thr		
260	265	270
Ala Ser Lys Ala Thr Ala Glu Ala Lys Pro Val Pro Ala Thr Ala Ser		
275	280	285
Leu Met Ala Thr Lys Val Thr Ala Glu Ala Lys Pro Ala Pro Ser Pro		
290	295	300
Ser Val Pro Lys Ala Thr Thr Asp Thr Lys Ala Val Thr Ala Thr Ala		
305	310	315
320		
Pro Lys Ala Gly Pro Asp Val Lys Pro Ala Val Ala Val Cys Ala Glu		
325	330	335
Ala Lys Pro Ala Pro Pro Pro Pro Gln Gln Leu Pro Lys Ala Ala		
340	345	350
Ala Ala Ala Ala Pro Thr Gly Thr Glu Leu Lys Pro Ala Thr Ala Pro		
355	360	365
Pro His Gly Ser Pro Arg Ala Asn Ser His Thr Val Thr Val Thr Pro		
370	375	380
Pro Asn Val Pro Arg Ala Ala Ala Thr Val Pro Thr Ala Gly Ala		

385	390	395	400
Val Pro Lys Ala Ser Thr Gly Thr Thr Pro Ala Ala Ala Pro Gln Gln			
405	410	415	
Pro Val Pro Lys Ala Ala Pro Val Thr Pro Pro Ser Pro Gln Gln Ala			
420	425	430	
Val Pro Arg Ala Ala Thr Ala Ala Ala Pro Val Thr Pro Gln Gln			
435	440	445	
Pro Val Thr Lys Ala Ala Thr Thr Thr Asn Ala Thr Pro Pro Pro Gln			
450	455	460	
Pro Ile Pro Lys Ala Ala Thr Thr Thr Ala Thr Pro Val Thr Pro			
465	470	475	480
Gln Gln Pro Ile Pro Lys Ala Gly Thr Asp Ala Ala Pro Pro Pro Ala			
485	490	495	
Val Pro Lys Ala Pro Ser Asp Gly Arg Ala Ala Thr Pro Gly Val Pro			
500	505	510	
Asn Ala Ala Thr Asp Pro Gln Lys Pro Pro Pro Thr Pro Gln Ser Val			
515	520	525	
Pro Ser Ala Val Thr Glu Pro Lys Pro Gln Pro Arg Ala Ala Pro Pro			
530	535	540	
Pro Ser Asn Glu Ala Thr Pro Ala Val Pro Ser Pro Ser Pro Asn Leu			
545	550	555	560
Lys Ser Pro Leu Pro Thr Ile Pro Lys Pro Val Pro Leu Met Ala Leu			
565	570	575	
Thr Pro Gln Pro Val Thr Ala Gln Met Val Thr Gln Leu Ala Ala Thr			
580	585	590	
Lys Pro Ser Pro Ile Val Pro Lys Ala Ser Pro Lys Ala Leu Met Thr			
595	600	605	
Pro Pro Pro Pro Pro Gly Leu Pro Arg Ala Leu Ala Ala Lys			
610	615	620	
Leu Leu Gly Leu Pro Ser Ser Pro Val Ala Ser Ala Met His Ala Lys			
625	630	635	640
Val Thr Pro Arg Pro Leu Pro Ala Ser Pro Val Pro Met Ala Ala Ser			

645 650 655

Pro Ala Ser Leu Gly Pro Asp Ala Ala Arg Val Ala Leu Ala Thr Asn
660 665 670

Ala Ala Ser Pro Gly Ala Lys Pro Glu Ala Ala Gly Gly Asn Gly Thr
675 680 685

Leu Met Ala Pro Met Gly Ala Ala Asn Thr Gln Met Ala Pro Ile Gly
690 695 700

Ala Ala Gly Ala Ala Gln Thr Ala Pro Met Gly Ala Ala His Thr His
705 710 715 720

Val Ser Pro Met Gly Ala Gly Gly Ala Thr Gln Met Ser Pro Thr Gly
725 730 735

Ala Ala Asn Thr His Met Ser Pro Ile Gly Ala Gly Gly Ala Thr Gln
740 745 750

Met Ser Pro Met Gly Ala Ala Asn Thr Gln Met Ser Pro Met Gly Ala
755 760 765

Thr Thr Thr Gln Met Ser Pro Met Gly Ala Ala Ala Thr Thr Gln Pro
770 775 780

Ser Pro Met Gly Ala Ala Ala Thr Gln Val Thr Ala Thr Ser Ala Gly
785 790 795 800

Asn Thr Met Gln Val Ser Pro Met Gly Ala Ala Thr Pro Pro Gln Thr
805 810 815

Pro Ser Val Gly Ala Ala Thr Thr Pro Gln Pro Ser Pro Met Gly Ala
820 825 830

Ala Thr Thr Leu Met Ser Pro Met Gly Ala Ala Thr Thr Pro Gln Pro
835 840 845

Ser Pro Met Gly Ala Val Thr Thr Gln Pro Pro Pro Met Ala Ala Thr
850 855 860

Asn Thr Thr Gln Pro Pro Pro Met Ala Ala Ser Thr Pro Gln Ser Thr
865 870 875 880

Pro Met Gly Ala Ala Thr Thr Gln Ser Pro Pro Met Gly Ala Thr
885 890 895

Thr Thr Gln Ser Pro Pro Met Gly Ala Ser Thr Pro Gln Ala Pro Pro

900 905 910

Thr Val Ala Gly Ser Pro Thr Pro Pro Pro Pro Ile Pro Pro Ser Pro
915 920 925

Thr Ala Gln Thr Ser Pro Gln Pro Met Ser Lys Ser Pro Pro Pro Asp
930 935 940

Pro Pro Lys Ala Pro Ser Ala Ala Ala Gln Thr Ser Pro Ala Ala His
945 950 955 960

Val Ala Asn Ala Ser Pro Gly Val Thr Ala Val Ser Pro Ala Pro Ile
965 970 975

Gly Val Thr Glu Ala Ser Pro Ser Ala Asp Gly Ala Arg Leu Ser Pro
980 985 990

Gly Pro Thr Ala Ala Thr Asp Gly Pro Lys Ala Ser Pro Ala Ala Thr
995 1000 1005

Ala Asp Val Thr Glu Ala Ala Thr Asp Val Thr Ala Ala Ala Thr Ala
1010 1015 1020

Val Pro Ala Glu Ala Ala Pro Thr Lys Ala Lys Arg Ser Ser Ser Ser
1025 1030 1035 1040

Ser
1045 1050 1055

Ser Ser Ser Ser Asp Ser Asp Ser Ser Ser Ser Ser Glu Ser Asn
1060 1065 1070

Pro Ala Ser Pro Ala Pro Ala Val Gly Asp Gly Gln Gln Gln Met Thr
1075 1080 1085

Pro Gly Ala Ala Gln Ser Val Pro Pro Val Thr Glu Ala Ala Val Gln
1090 1095 1100

Glu Ala Ala Ala Ala Ala Ala Ala Gly Ala Glu Arg Glu Gly
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Arg Pro Thr Arg Arg Lys Lys Arg Thr Arg Ser Ser Ser Ser Ser Ser
1125 1130 1135

Ser
1140 1145 1150

<210> 80
<211> 199
<212> PRT
<213> Homo sapiens

<400> 80
Met Asn Cys Val Cys Arg Leu Val Leu Val Val Leu Ser Leu Trp Pro
1 5 10 15

Asp Thr Ala Val Ala Pro Gly Pro Pro Pro Gly Pro Pro Arg Val Ser
20 25 30

Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg Ser
35 40 45

Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe
50 55 60

Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala Met
65 70 75 80

Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr Arg
85 90 95

Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu Arg
100 105 110

Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr
115 120 125

Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu Met
130 135 140

Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro
145 150 155 160

Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His Ala
165 170 175

Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly Leu
180 185 190

Leu Leu Leu Lys Thr Arg Leu
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<210> 81
<211> 1029

<212> DNA

<213> Homo sapiens

<400> 81

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aatggcagtg gagtggtgt gtggccacca gtggagactg tgggctggc acacgggagg 600
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aaaaagatgtc acctgtggaa cataaaaagg acatcagcaa acaggatcag ttaactattg 960
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caaaaacaa 1029

<210> 82

<211> 216

<212> PRT

<213> Homo sapiens

<400> 82

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 83
<211> 346
<212> PRT
<213> Rattus norvegicus

<400> 83
Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr
100 105 110

Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala Met
115 120 125

Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser Ser
130 135 140

Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp Ala
145 150 155 160

Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr Tyr Gln Arg Leu Phe
165 170 175

His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu His Trp Pro Asn Gln
180 185 190

Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr Leu
195 200 205

Leu Pro Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His
210 215 220

Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys
225 230 235 240

Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Phe Gly Ile
245 250 255

Ser Trp Leu Pro His His Val Ile His Leu Trp Ala Glu Phe Gly Ala
260 265 270

Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His Cys
275 280 285

Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe Leu
290 295 300

Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys Arg Val
305 310 315 320

Cys Asn Glu Ser Pro His Gly Asp Ala Lys Glu Lys Asn Arg Ile Asp
325 330 335

Thr Pro Pro Ser Thr Asn Cys Thr His Val
340 345

<210> 84
<211> 1308
<212> DNA
<213> Bos taurus

<400> 84
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ccgaggccgc aggaggagcc ccagcggcgg cgcacagc agcctgaagc tcggagcct 180
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acccggacg ctgggcctcg gtcgcgcgc cctggccgc ggcggcgcac ggccttcggc 960
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<210> 85
<211> 436
<212> PRT
<213> Bos taurus

<400> 85
Arg Ala Ser Ala Glu Leu Gly Ser Ala Lys Gly Met Arg Thr Arg Lys
1 5 10 15

Glu Gly Arg Met Pro Arg Ala Pro Arg Glu Asn Ala Thr Ala Arg Glu
20 25 30

Pro Leu Asp Arg Gln Glu Pro Pro Pro Arg Pro Gln Glu Glu Pro Gln
35 40 45

Arg Arg Pro Pro Gln Gln Pro Glu Ala Arg Glu Pro Pro Gly Arg Gly

50

55

60

Pro Arg Leu Val Pro His Glu Tyr Met Leu Ser Ile Tyr Arg Thr Tyr
65 70 75 80

Ser Ile Ala Glu Lys Leu Gly Ile Asn Ala Ser Phe Phe Gln Ser Ser
85 90 95

Lys Ser Ala Asn Thr Ile Thr Ser Phe Val Asp Arg Gly Leu Asp Asp
100 105 110

Leu Ser His Thr Pro Leu Arg Arg Gln Lys Tyr Leu Phe Asp Val Ser
115 120 125

Thr Leu Ser Asp Lys Glu Glu Leu Val Gly Ala Asp Val Arg Leu Phe
130 135 140

Arg Gln Ala Pro Ala Ala Leu Ala Pro Pro Ala Ala Ala Pro Leu Ala
145 150 155 160

Ala Leu Arg Leu Pro Val Ala Pro Ala Ala Gly Ser Ala Glu Pro Gly
165 170 175

Pro Ala Gly Ala Pro Arg Pro Gly Trp Glu Val Phe Asp Val Trp Arg
180 185 190

Gly Leu Arg Pro Gln Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala
195 200 205

Ala Trp Gly Gly Glu Pro Gly Ala Ala Glu Asp Glu Ala Arg Thr Pro
210 215 220

Gly Pro Gln Gln Pro Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly
225 230 235 240

Arg Arg Val Arg Thr Pro Gln Glu Arg Ala Leu Leu Val Val Phe Ser
245 250 255

Arg Ser Gln Arg Lys Thr Leu Phe Ala Glu Met Arg Glu Gln Leu Gly
260 265 270

Ser Ala Thr Glu Val Val Gly Pro Gly Gly Ala Glu Gly Ser Gly
275 280 285

Pro Pro Pro Pro Pro Pro Pro Pro Ser Gly Thr Pro Asp Ala
290 295 300

Gly Leu Trp Ser Pro Ser Pro Gly Arg Arg Arg Arg Thr Ala Phe Ala

305

310

315

320

Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser
325 330 335

Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp
340 345 350

Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys
355 360 365

Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile
370 375 380

Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys
385 390 395 400

Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala
405 410 415

Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val Glu Ser
420 425 430

Cys Gly Cys Arg
435